

SEQUENCE LISTING

<110> Messier, Walter

<120> Methods to Identify Evolutionarily Significant Changes in Polynucleotide and Polypeptide Sequences in Domesticated Plants

<130> GENO200.1/CIP

<150> US 09/240,915

<151> 1999-01-29

<150> US 60/349,088

<151> 2002-01-16

<150> US 09/368,810

<151> 1999-08-03

<150> US 09/875,666

<151> 2001-06-06

<150> US 60/315,595

<151> 2001-08-29

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<170> PatentIn version 3.1

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Glu Met Leu Ala Asn Val Gly Pro Ser Pro Ser Lys Ala Lys Gln Ile
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gctgaccgtg gaaagaggat attactgacc ttcggtttgc taattttgg tgtgccgttg	360
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aattgtggat gtaagagtct gcagttgtta aaatctggaa acagcacatt ttgccgtagt	540
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ctatgaagta acatgaacag tttgtatgta ttctgttgat gcataactgc attatttgtg	720
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ggtgattttc aagcagtact gaaacaaggt atgccaaccc cagcaaaagt catgccaaga	1740
gtcgatgttc ctccatctat gagggcatca aaggaaaggg ttggccttcg tctgcagag	1800

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atgttgGCCA atgttggtcc ttcacccatcc aaggcaaaac agattgtcaa tcctgcagct 1860
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ctgttgccat ccaaggTTca tatagatgct actcgatctt ttacgaaggT ctcccagaca 1980
gagatcaagc cggaagtaca gcccCCAatt ccgaaggTgc ctgtggctat gcctaccatc 2040
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gctgaagctg cttcagtatc agtagagaag cagtCCAagT cagatcgcaa aaagagccgc 2160
aaggctgaga agaaagagaa gaagttcaaa gatttatttg ttacctggga tcctccgtct 2220
atggaaatgg atgatatgga tcttggggac caggattggc tgcttggtag tacgaggaaa 2280
cctgatgctg gcattggcaa ctgcagagaa attgttgatc cacttacttc tcaatcagca 2340
gagcagttct cattgcagcc tagggcgatt catttaccag accttcatgt ctatcagttg 2400
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t 2461

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<210> 8
<211> 1341
<212> DNA
<213> Oryza sativa cv. Teqing

<220>
<221> CDS
<222> (1)..(1341)
<223>

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Met Ser Arg Cys Phe Pro Tyr Pro Pro Pro Gly Tyr Val Arg Asn Pro
1 5 10 15

gtg gtg gcc gtg gcc gcg gcc gaa gcg cag gcg acc act aag ctc cag 96
Val Val Ala Val Ala Ala Ala Glu Ala Gln Ala Thr Thr Lys Leu Gln
20 25 30

aaa gaa agg gaa aag gcc gaa aag aag aaa gag aaa aag agt gac agg 144
Lys Glu Arg Glu Lys Ala Glu Lys Lys Lys Glu Lys Lys Ser Asp Arg
35 40 45

aaa gct ctt cca cat ggt gag ata tcc aag cat tca aag cga acc cac 192
Lys Ala Leu Pro His Gly Glu Ile Ser Lys His Ser Lys Arg Thr His
50 55 60

aag aag aga aaa cat gaa gac atc aat aat gct gat cag aag tcc cgg 240
Lys Lys Arg Lys His Glu Asp Ile Asn Asn Ala Asp Gln Lys Ser Arg
65 70 75 80

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aag gtt tcc tcc atg gaa cct ggt gag caa ttg gag aag agt gga ctc Lys Val Ser Ser Met Glu Pro Gly Glu Gln Leu Glu Lys Ser Gly Leu 85 90 95	288
tca gaa gag cat gga gct cct tgc ttt act cag aca gtg cat ggc tct Ser Glu Glu His Gly Ala Pro Cys Phe Thr Gln Thr Val His Gly Ser 100 105 110	336
cca gag agt tca cag gac agc agc aag aga aga aag gtt gtg tta ccc Pro Glu Ser Ser Gln Asp Ser Ser Lys Arg Arg Lys Val Val Leu Pro 115 120 125	384
agt cct agc caa gct aag aat ggt aac atc ctt cga ata aag ata aga Ser Pro Ser Gln Ala Lys Asn Gly Asn Ile Leu Arg Ile Lys Ile Arg 130 135 140	432
aga gat caa gat tct tca gct tcc ctt tcg gag aaa tct aat gtt gta Arg Asp Gln Asp Ser Ser Ala Ser Leu Ser Glu Lys Ser Asn Val Val 145 150 155 160	480
caa aca cca gtt cat caa atg gga tca gtt tca tct ctg cca agt aag Gln Thr Pro Val His Gln Met Gly Ser Val Ser Ser Leu Pro Ser Lys 165 170 175	528
aaa aac tca atg caa cca cac aac acc gaa atg atg gtg aga aca gca Lys Asn Ser Met Gln Pro His Asn Thr Glu Met Met Val Arg Thr Ala 180 185 190	576
tca acc cag cag caa agc atc aaa ggt gat ttt caa gca gta ctg aaa Ser Thr Gln Gln Gln Ser Ile Lys Gly Asp Phe Gln Ala Val Leu Lys 195 200 205	624
caa ggt atg cca acc cca gca aaa gtc atg cca aga gtc gat gtt cct Gln Gly Met Pro Thr Pro Ala Lys Val Met Pro Arg Val Asp Val Pro 210 215 220	672
cca tct atg agg gca tca aag gaa agg gtt ggc ctt cgt cct gca gag Pro Ser Met Arg Ala Ser Lys Glu Arg Val Gly Leu Arg Pro Ala Glu 225 230 235 240	720
atg ttg gcc aat gtt ggt cct tca cca tcc aag gca aaa cag att gtc Met Leu Ala Asn Val Gly Pro Ser Pro Ser Lys Ala Lys Gln Ile Val 245 250 255	768
aat cct gca gct gct aag gtt aca caa aga gtt gat cct cca cct gcc Asn Pro Ala Ala Lys Val Thr Gln Arg Val Asp Pro Pro Pro Ala 260 265 270	816
aag gca tct cag aga att gat cct ctg ttg cca tcc aag gtt cat ata Lys Ala Ser Gln Arg Ile Asp Pro Leu Leu Pro Ser Lys Val His Ile 275 280 285	864
gat gct act cga tct ttt acg aag gtc tcc cag aca gag atc aag ccg Asp Ala Thr Arg Ser Phe Thr Lys Val Ser Gln Thr Glu Ile Lys Pro 290 295 300	912
gaa gta cag ccc cca att ccg aag gtg cct gtg gct atg cct acc atc	960

Glu Val Gln Pro Pro Ile Pro Lys Val Pro Val Ala Met Pro Thr Ile
305 310 315 320

aat cgt cag cag att gac acc tcg cag ccc aaa gaa gag cct tgc tcc 1008
Asn Arg Gln Gln Ile Asp Thr Ser Gln Pro Lys Glu Glu Pro Cys Ser
325 330 335

tct ggc agg aat gct gaa gct gct tca gta tca gta gag aag cag tcc 1056
Ser Gly Arg Asn Ala Glu Ala Ala Ser Val Ser Val Glu Lys Gln Ser
340 345 350

aag tca gat cgc aaa aag agc cgc aag gct gag aag aaa gag aag aag 1104
Lys Ser Asp Arg Lys Lys Ser Arg Lys Ala Glu Lys Lys Glu Lys Lys
355 360 365

ttc aaa gat tta ttt gtt acc tgg gat cct ccg tct atg gaa atg gat 1152
Phe Lys Asp Leu Phe Val Thr Trp Asp Pro Pro Ser Met Glu Met Asp
370 375 380

gat atg gat ctt ggg gac cag gat tgg ctg ctt ggt agt acg agg aaa 1200
Asp Met Asp Leu Gly Asp Gln Asp Trp Leu Leu Gly Ser Thr Arg Lys
385 390 395 400

cct gat gct ggc att ggc aac tgc aga gaa att gtt gat cca ctt act 1248
Pro Asp Ala Gly Ile Gly Asn Cys Arg Glu Ile Val Asp Pro Leu Thr
405 410 415

tct caa tca gca gag cag ttc tca ttg cag cct agg gcg att cat tta 1296
Ser Gln Ser Ala Glu Gln Phe Ser Leu Gln Pro Arg Ala Ile His Leu
420 425 430

cca gac ctt cat gtc tat cag ttg cca tat gtg gtt cca ttc tag 1341
Pro Asp Leu His Val Tyr Gln Leu Pro Tyr Val Val Pro Phe
435 440 445

<210> 9

<211> 446

<212> PRT

<213> Oryza sativa cv. Teqing

<400> 9

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20 25 30

Lys Glu Arg Glu Lys Ala Glu Lys Lys Lys Glu Lys Lys Ser Asp Arg
35 40 45

Lys Ala Leu Pro His Gly Glu Ile Ser Lys His Ser Lys Arg Thr His
50 55 60

Lys Lys Arg Lys His Glu Asp Ile Asn Asn Ala Asp Gln Lys Ser Arg
65 70 75 80

Lys Val Ser Ser Met Glu Pro Gly Glu Gln Leu Glu Lys Ser Gly Leu
85 90 95

Ser Glu Glu His Gly Ala Pro Cys Phe Thr Gln Thr Val His Gly Ser
100 105 110

Pro Glu Ser Ser Gln Asp Ser Ser Lys Arg Arg Lys Val Val Leu Pro
115 120 125

Ser Pro Ser Gln Ala Lys Asn Gly Asn Ile Leu Arg Ile Lys Ile Arg
130 135 140

Arg Asp Gln Asp Ser Ser Ala Ser Leu Ser Glu Lys Ser Asn Val Val
145 150 155 160

Gln Thr Pro Val His Gln Met Gly Ser Val Ser Ser Leu Pro Ser Lys
165 170 175

Lys Asn Ser Met Gln Pro His Asn Thr Glu Met Met Val Arg Thr Ala
180 185 190

Ser Thr Gln Gln Gln Ser Ile Lys Gly Asp Phe Gln Ala Val Leu Lys
195 200 205

Gln Gly Met Pro Thr Pro Ala Lys Val Met Pro Arg Val Asp Val Pro
210 215 220

Pro Ser Met Arg Ala Ser Lys Glu Arg Val Gly Leu Arg Pro Ala Glu
225 230 235 240

Met Leu Ala Asn Val Gly Pro Ser Pro Ser Lys Ala Lys Gln Ile Val
245 250 255

Asn Pro Ala Ala Ala Lys Val Thr Gln Arg Val Asp Pro Pro Pro Ala
260 265 270

Lys Ala Ser Gln Arg Ile Asp Pro Leu Leu Pro Ser Lys Val His Ile
275 280 285

206T20 2405200T

Asp Ala Thr Arg Ser Phe Thr Lys Val Ser Gln Thr Glu Ile Lys Pro
290 295 300

Glu Val Gln Pro Pro Ile Pro Lys Val Pro Val Ala Met Pro Thr Ile
305 310 315 320

Asn Arg Gln Gln Ile Asp Thr Ser Gln Pro Lys Glu Glu Pro Cys Ser
325 330 335

Ser Gly Arg Asn Ala Glu Ala Ala Ser Val Ser Val Glu Lys Gln Ser
340 345 350

Lys Ser Asp Arg Lys Lys Ser Arg Lys Ala Glu Lys Lys Glu Lys Lys
355 360 365

Phe Lys Asp Leu Phe Val Thr Trp Asp Pro Pro Ser Met Glu Met Asp
370 375 380

Asp Met Asp Leu Gly Asp Gln Asp Trp Leu Leu Gly Ser Thr Arg Lys
385 390 395 400

Pro Asp Ala Gly Ile Gly Asn Cys Arg Glu Ile Val Asp Pro Leu Thr
405 410 415

Ser Gln Ser Ala Glu Gln Phe Ser Leu Gln Pro Arg Ala Ile His Leu
420 425 430

Pro Asp Leu His Val Tyr Gln Leu Pro Tyr Val Val Pro Phe
435 440 445

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<211> 451
<212> DNA
<213> Oryza sativa cv. Lemont

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tcgggggttcc ccttacgatt cgcgggcgga ttagcgcgag gcgcgcctcc ccctacctct 120
gtgtgatccg ggggtgaggt taggcgggac gccggggcat cagccatgtc gaggtgcttc 180
ccctaccgcg cgccggggta cgtgcgaaac ccagtgggtg ccgtggccgc ggccgaagcg 240
caggcgacca ctaaggtttg ttgaaccatc ggatttacac acgcacgtgc cggatcattt 300

gctcttgccct gttgggttttg atcggatctg ttgggtgtggo gtgtgtgatt tggggatcgc 360
acgtgcggggg aagctaacct ttgcatggat aacttgagat ttgtgaggcc gcgcttcgac 420
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<210> 11
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<212> DNA
<213> Oryza sativa cv. Lemont

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agaagaaaga gaaaaggagt gacaggaaag ctcttcacaca tggtagata tccaagcatt 300
caaagcgaac ccaccacaag aagagaaaac atgaagacat caataatgct gatcagaagt 360
cccgaagggt ttcttccatg gaacctggtg agcaattgga gaagagtgga ctctcagaag 420
agcatggagc tccttgcttt actcagacag agcatggctc tccagagagt tcacaggaca 480
gcagcaagag aagaaagggt gtgttaccca gtcctagcca agctaagaat ggtgaggccc 540
tttcttgcat ttgtcttctt ttagctgggt atgttgaatt ggtttgactt atcctgaatt 600
atcatcttgc aggtaacatc cttcgaataa agataagaag agatcaagat tcttcagctt 660
ccctttcgga gaaatctaatt gttgtacaaa caccagttca tcaaagggga tcagtttcat 720
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caaccccagc aaaagtcattg ccaagagtcg atgttctctc atctatgagg gcatcaaagg 900
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gatcttttac gaaggctctcc cagacagaga tcaagccgga agtacagccc ccaattctga 1140
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aagagccttg ctctctctggc aggaatgctg aagctgcttc agtatcagta gagaagcagt 1260
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tatttggttac ctgggacacct ccgtctatgg aaatggatga tatggatctc ggggaccagg 1380
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taccagacct tcatgtctat cagttgccat atgtggttcc attctagggtt tgtgtagtga 1560
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<212> DNA
<213> Oryza sativa cv. Lemont

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<222> (1)..(1344)
<223>

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gtg gtg gcc gtg gcc gcg gcc gaa gcg cag gcg acc act aag ctc cag 96
Val Val Ala Val Ala Ala Ala Glu Ala Gln Ala Thr Thr Lys Leu Gln
20 25 30
aaa gaa agg gaa aag gct gaa aag aag aaa gag aaa agg agt gac agg 144
Lys Glu Arg Glu Lys Ala Glu Lys Lys Lys Glu Lys Arg Ser Asp Arg
35 40 45
aaa gct ctt cca cat ggt gag ata tcc aag cat tca aag cga acc cac 192
Lys Ala Leu Pro His Gly Glu Ile Ser Lys His Ser Lys Arg Thr His
50 55 60
cac aag aag aga aaa cat gaa gac atc aat aat gct gat cag aag tcc 240
His Lys Lys Arg Lys His Glu Asp Ile Asn Asn Ala Asp Gln Lys Ser
65 70 75 80
cgg aag gtt tcc tcc atg gaa cct ggt gag caa ttg gag aag agt gga 288
Arg Lys Val Ser Ser Met Glu Pro Gly Glu Gln Leu Glu Lys Ser Gly
85 90 95
ctc tca gaa gag cat gga gct cct tgc ttt act cag aca gag cat ggc 336
Leu Ser Glu Glu His Gly Ala Pro Cys Phe Thr Gln Thr Glu His Gly
100 105 110
tct cca gag agt tca cag gac agc agc aag aga aga aag gtt gtg tta 384
Ser Pro Glu Ser Ser Gln Asp Ser Ser Lys Arg Arg Lys Val Val Leu
115 120 125
ccc agt cct agc caa gct aag aat ggt aac atc ctt cga ata aag ata 432
Pro Ser Pro Ser Gln Ala Lys Asn Gly Asn Ile Leu Arg Ile Lys Ile

130	135	140	
aga aga gat caa gat tct tca gct tcc ctt tcg gag aaa tct aat gtt			480
Arg Arg Asp Gln Asp Ser Ser Ala Ser Leu Ser Glu Lys Ser Asn Val			
145	150	155	160
gta caa aca cca gtt cat caa atg gga tca gtt tca tct ctg cca agt			528
Val Gln Thr Pro Val His Gln Met Gly Ser Val Ser Ser Leu Pro Ser			
	165	170	175
aag aaa aac tca atg caa cca cac aac acc gaa atg atg gtg aga aca			576
Lys Lys Asn Ser Met Gln Pro His Asn Thr Glu Met Met Val Arg Thr			
	180	185	190
gca tca acc cag cag caa agc atc aaa ggt gat ttt caa gca gta ccg			624
Ala Ser Thr Gln Gln Gln Ser Ile Lys Gly Asp Phe Gln Ala Val Pro			
	195	200	205
aaa caa ggt atg cca acc cca gca aaa gtc atg cca aga gtc gat gtt			672
Lys Gln Gly Met Pro Thr Pro Ala Lys Val Met Pro Arg Val Asp Val			
	210	215	220
cct cca tct atg agg gca tca aag gaa agg att ggc ctt cgt cct gca			720
Pro Pro Ser Met Arg Ala Ser Lys Glu Arg Ile Gly Leu Arg Pro Ala			
	225	230	240
gag atg ttg gcc aat gtt ggt cct tca ccc tcc aag gca aaa cag att			768
Glu Met Leu Ala Asn Val Gly Pro Ser Pro Ser Lys Ala Lys Gln Ile			
	245	250	255
gtc aat cct gca gct gct aag gtt aca caa aga gtt gat cct cca cct			816
Val Asn Pro Ala Ala Ala Lys Val Thr Gln Arg Val Asp Pro Pro Pro			
	260	265	270
gcc aag gca tct cag aga att gat cct ctg ttg cca tcc aag gtt cat			864
Ala Lys Ala Ser Gln Arg Ile Asp Pro Leu Leu Pro Ser Lys Val His			
	275	280	285
ata gat gct act cga tct ttt acg aag gtc tcc cag aca gag atc aag			912
Ile Asp Ala Thr Arg Ser Phe Thr Lys Val Ser Gln Thr Glu Ile Lys			
	290	295	300
ccg gaa gta cag ccc cca att ctg aag gtg cct gtg gct atg cct acc			960
Pro Glu Val Gln Pro Pro Ile Leu Lys Val Pro Val Ala Met Pro Thr			
	305	310	315
atc aat cgt cag cag att gac acc tcg cag ccc aaa gaa gag cct tgc			1008
Ile Asn Arg Gln Gln Ile Asp Thr Ser Gln Pro Lys Glu Glu Pro Cys			
	325	330	335
tcc tct ggc agg aat gct gaa gct gct tca gta tca gta gag aag cag			1056
Ser Ser Gly Arg Asn Ala Glu Ala Ala Ser Val Ser Val Glu Lys Gln			
	340	345	350
tcc aag tca gat cgc aaa aag agc cgc aag gct gag aag aaa gag aag			1104
Ser Lys Ser Asp Arg Lys Lys Ser Arg Lys Ala Glu Lys Lys Glu Lys			
	355	360	365

aag ttc aaa gat tta ttt gtt acc tgg gat cct ccg tct atg gaa atg 1152
 Lys Phe Lys Asp Leu Phe Val Thr Trp Asp Pro Pro Ser Met Glu Met
 370 375 380

gat gat atg gat ctc ggg gac cag gat tgg ctg ctt gat agt acg agg 1200
 Asp Asp Met Asp Leu Gly Asp Gln Asp Trp Leu Leu Asp Ser Thr Arg
 385 390 395 400

aaa cct gat gct ggc att ggc aac tgc aga gaa att gtt gat cca ctt 1248
 Lys Pro Asp Ala Gly Ile Gly Asn Cys Arg Glu Ile Val Asp Pro Leu
 405 410 415

act tct caa tca gca gag cag ttc tca ttg cag cct agg gcg att cat 1296
 Thr Ser Gln Ser Ala Glu Gln Phe Ser Leu Gln Pro Arg Ala Ile His
 420 425 430

tta cca gac ctt cat gtc tat cag ttg cca tat gtg gtt cca ttc tag 1344
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 435 440 445

<210> 13

<211> 447

<212> PRT

<213> Oryza sativa cv. Lemont

<400> 13

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 20 25 30

Lys Glu Arg Glu Lys Ala Glu Lys Lys Lys Glu Lys Arg Ser Asp Arg
 35 40 45

Lys Ala Leu Pro His Gly Glu Ile Ser Lys His Ser Lys Arg Thr His
 50 55 60

His Lys Lys Arg Lys His Glu Asp Ile Asn Asn Ala Asp Gln Lys Ser
 65 70 75 80

Arg Lys Val Ser Ser Met Glu Pro Gly Glu Gln Leu Glu Lys Ser Gly
 85 90 95

Leu Ser Glu Glu His Gly Ala Pro Cys Phe Thr Gln Thr Glu His Gly
 100 105 110

Ser Pro Glu Ser Ser Gln Asp Ser Ser Lys Arg Arg Lys Val Val Leu
 115 120 125

Pro Ser Pro Ser Gln Ala Lys Asn Gly Asn Ile Leu Arg Ile Lys Ile
 130 135 140

Arg Arg Asp Gln Asp Ser Ser Ala Ser Leu Ser Glu Lys Ser Asn Val
 145 150 155 160

Val Gln Thr Pro Val His Gln Met Gly Ser Val Ser Ser Leu Pro Ser
 165 170 175

Lys Lys Asn Ser Met Gln Pro His Asn Thr Glu Met Met Val Arg Thr
 180 185 190

Ala Ser Thr Gln Gln Gln Ser Ile Lys Gly Asp Phe Gln Ala Val Pro
 195 200 205

Lys Gln Gly Met Pro Thr Pro Ala Lys Val Met Pro Arg Val Asp Val
 210 215 220

Pro Pro Ser Met Arg Ala Ser Lys Glu Arg Ile Gly Leu Arg Pro Ala
 225 230 235 240

Glu Met Leu Ala Asn Val Gly Pro Ser Pro Ser Lys Ala Lys Gln Ile
 245 250 255

Val Asn Pro Ala Ala Ala Lys Val Thr Gln Arg Val Asp Pro Pro Pro
 260 265 270

Ala Lys Ala Ser Gln Arg Ile Asp Pro Leu Leu Pro Ser Lys Val His
 275 280 285

Ile Asp Ala Thr Arg Ser Phe Thr Lys Val Ser Gln Thr Glu Ile Lys
 290 295 300

Pro Glu Val Gln Pro Pro Ile Leu Lys Val Pro Val Ala Met Pro Thr
 305 310 315 320

Ile Asn Arg Gln Gln Ile Asp Thr Ser Gln Pro Lys Glu Glu Pro Cys
 325 330 335

Ser Ser Gly Arg Asn Ala Glu Ala Ala Ser Val Ser Val Glu Lys Gln

340

345

350

Ser Lys Ser Asp Arg Lys Lys Ser Arg Lys Ala Glu Lys Lys Glu Lys
 355 360 365

Lys Phe Lys Asp Leu Phe Val Thr Trp Asp Pro Pro Ser Met Glu Met
 370 375 380

Asp Asp Met Asp Leu Gly Asp Gln Asp Trp Leu Leu Asp Ser Thr Arg
 385 390 395 400

Lys Pro Asp Ala Gly Ile Gly Asn Cys Arg Glu Ile Val Asp Pro Leu
 405 410 415

Thr Ser Gln Ser Ala Glu Gln Phe Ser Leu Gln Pro Arg Ala Ile His
 420 425 430

Leu Pro Asp Leu His Val Tyr Gln Leu Pro Tyr Val Val Pro Phe
 435 440 445

<210> 14

<211> 2459

<212> DNA

<213> Oryza sativa strain IR64

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 attactgacc ttcggtttgc taattttggt tgtgccgttg aatctgaaat aaccagaata 360
 gtcattggga aaaagtctga tctggaaggt tcgaattaca tttctatata ttgttgtgct 420
 cccagacgat ggttgcaaga aattactcat gctggataaa attgtggatg taagagtctg 480
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 tctcgttatt ggtgtgttac gagtaacctg tgtgttgta tctccgcttg gactagattc 600
 caagtaatcc agtgccttca tgacctgcaa attctatgcc tatgaagtaa catgaacagt 660
 ttgtatgtat tctgttgatg catacttgca ttatttgta gatgtacatg ttgtggtaaa 720

attttgcatt caccatatag aaatagtaat tgactatcct tgttttagttc gaaaactact	780
gcaggtttag ttattctctg ttgccaagag tgcttggtat gattgtaagg gttacagttc	840
tgtgactaac catgtaacaa atatattaag gattatcaaa ttattctatg tgaagtgtcc	900
gtgccctaata tgtgttatct tctgtaactg atagcacaac atttgtttcc tgctgtgtgc	960
ttgtgtaaat tgggtacttca tcattactat atatttcaaa gaaaattctg cattgcattc	1020
ccgtcgtccg ttctaaatca gaactgacga ttgctctggt ggctgaagct ccagaaagaa	1080
agggaaaagg ccgaaaagaa gaaagagaaa aggagtgaca ggaaagctct tccacatggt	1140
gagatatcca agcattcaaa gcgaacccac aagaagagaa aacatgaaga catcaataat	1200
gctgatcaga agtcccggaa ggtttcctcc atggaacctg gtgagcaatt ggagaagagt	1260
ggactctcag aagagcatgg agctccttgc tttactcaga cagtgcattg ctctccagag	1320
agttcacagg acagcagcaa gagaagaaag gttgtgttac ccagtcctag ccaagctaag	1380
aatggtgagg ccctttcttg catttgtctt ctttttagctg gtgatgttga attggtttga	1440
cttatcctga attatcatct tgcaggtaac atccttcgaa taaagataag aagagatcaa	1500
gattcttcag cttccctttc ggagaaatct aatggtgtac aaacaccagt tcatcaaagt	1560
ggatcagttt catctctgcc aagtaagaaa aactcaatgc aaccacacaa caccgaaatg	1620
atggtgagaa cagcatcaac ccagcagcaa agcatcaaag gtgattttca agcagtactg	1680
aaacaaggta tgccaacccc agcaaaagtc atgccaagag tcgatgttcc tccatctatg	1740
agggcaccaa aggaaagggg tggccttcgt cctgcagaga tgttggccaa tgttggtcct	1800
tcaccctcca aggcaaaaca gattgtcaat cctgcagctg ctaaggttac acaaagagtt	1860
gatcctccac ctgccaaggc atctcagaga attgatcctc tgttgccatc caaggttcat	1920
atagatgcta ctgatcttt tacgaagctc tcccagacag agatcaagcc ggaagtacag	1980
cccccaattc cgaagggtgc tgtggctatg cctaccatca atcgtcagca gattgacacc	2040
tcgcagccca aagaagagcc ttgctcctct ggcaggaatg ctgaagctgc ttcagtatca	2100
gtagagaagc agtccaagtc agatcgcaaa aagagccgca aggctgagaa gaaagagaag	2160
aagttcaaag atttatttgt tacctgggat cctccgtcta tggaaatgga tgatatggat	2220
cttggggacc aggattggct gcttggtagt acgaggaaac ctgatgctgg cattggcaac	2280
tgcagagaaa ttgttgatcc acttacttct caatcagcgg agcagttctc attgcagcct	2340
agggcgattc atttaccaga cttcatgtc tatcagttgc catatgtggg tccattctag	2400
gtttgtgtag tgagatggag taggtgagaa gtagagagat gttgggagag agctgtgtg	2459

<210> 15
 <211> 1341
 <212> DNA
 <213> Oryza sativa strain IR64

<220>
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 <222> (1)..(1341)
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<400> 15
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 Met Ser Arg Cys Phe Pro Tyr Pro Pro Pro Gly Tyr Val Arg Asn Pro
 1 5 10 15

gtg gtg gcc gtg gcc gcg gcc gaa gcg cag gcg acc act aag ctc cag 96
 Val Val Ala Val Ala Ala Ala Glu Ala Gln Ala Thr Thr Lys Leu Gln
 20 25 30

aaa gaa agg gaa aag gcc gaa aag aag aaa gag aaa agg agt gac agg 144
 Lys Glu Arg Glu Lys Ala Glu Lys Lys Lys Glu Lys Arg Ser Asp Arg
 35 40 45

aaa gct ctt cca cat ggt gag ata tcc aag cat tca aag cga acc cac 192
 Lys Ala Leu Pro His Gly Glu Ile Ser Lys His Ser Lys Arg Thr His
 50 55 60

aag aag aga aaa cat gaa gac atc aat aat gct gat cag aag tcc cg 240
 Lys Lys Arg Lys His Glu Asp Ile Asn Asn Ala Asp Gln Lys Ser Arg
 65 70 75 80

aag gtt tcc tcc atg gaa cct ggt gag caa ttg gag aag agt gga ctc 288
 Lys Val Ser Ser Met Glu Pro Gly Glu Gln Leu Glu Lys Ser Gly Leu
 85 90 95

tca gaa gag cat gga gct cct tgc ttt act cag aca gtg cat ggc tct 336
 Ser Glu Glu His Gly Ala Pro Cys Phe Thr Gln Thr Val His Gly Ser
 100 105 110

cca gag agt tca cag gac agc agc aag aga aga aag gtt gtg tta ccc 384
 Pro Glu Ser Ser Gln Asp Ser Ser Lys Arg Arg Lys Val Val Leu Pro
 115 120 125

agt cct agc caa gct aag aat ggt aac atc ctt cga ata aag ata aga 432
 Ser Pro Ser Gln Ala Lys Asn Gly Asn Ile Leu Arg Arg Ile Lys Ile Arg
 130 135 140

aga gat caa gat tct tca gct tcc ctt tcg gag aaa tct aat gtt gta 480
 Arg Asp Gln Asp Ser Ser Ala Ser Leu Ser Glu Lys Ser Asn Val Val
 145 150 155 160

caa aca cca gtt cat caa atg gga tca gtt tca tct ctg cca agt aag 528
 Gln Thr Pro Val His Gln Met Gly Ser Val Ser Ser Leu Pro Ser Lys
 165 170 175

aaa aac tca atg caa cca cac aac acc gaa atg atg gtg aga aca gca Lys Asn Ser Met Gln Pro His Asn Thr Glu Met Met Val Arg Thr Ala 180 185 190	576
tca acc cag cag caa agc atc aaa ggt gat ttt caa gca gta ctg aaa Ser Thr Gln Gln Gln Ser Ile Lys Gly Asp Phe Gln Ala Val Leu Lys 195 200 205	624
caa ggt atg cca acc cca gca aaa gtc atg cca aga gtc gat gtt cct Gln Gly Met Pro Thr Pro Ala Lys Val Met Pro Arg Val Asp Val Pro 210 215 220	672
cca tct atg agg gca tca aag gaa agg gtt ggc ctt cgt cct gca gag Pro Ser Met Arg Ala Ser Lys Glu Arg Val Gly Leu Arg Pro Ala Glu 225 230 235 240	720
atg ttg gcc aat gtt ggt cct tca ccc tcc aag gca aaa cag att gtc Met Leu Ala Asn Val Gly Pro Ser Pro Ser Lys Ala Lys Gln Ile Val 245 250 255	768
aat cct gca gct gct aag gtt aca caa aga gtt gat cct cca cct gcc Asn Pro Ala Ala Ala Lys Val Thr Gln Arg Val Asp Pro Pro Pro Ala 260 265 270	816
aag gca tct cag aga att gat cct ctg ttg cca tcc aag gtt cat ata Lys Ala Ser Gln Arg Ile Asp Pro Leu Leu Pro Ser Lys Val His Ile 275 280 285	864
gat gct act cga tct ttt acg aag ctc tcc cag aca gag atc aag ccg Asp Ala Thr Arg Ser Phe Thr Lys Leu Ser Gln Thr Glu Ile Lys Pro 290 295 300	912
gaa gta cag ccc cca att ccg aag gtg cct gtg gct atg cct acc atc Glu Val Gln Pro Pro Ile Pro Lys Val Pro Val Ala Met Pro Thr Ile 305 310 315 320	960
aat cgt cag cag att gac acc tcg cag ccc aaa gaa gag cct tgc tcc Asn Arg Gln Gln Ile Asp Thr Ser Gln Pro Lys Glu Glu Pro Cys Ser 325 330 335	1008
tct ggc agg aat gct gaa gct gct tca gta tca gta gag aag cag tcc Ser Gly Arg Asn Ala Glu Ala Ala Ser Val Ser Val Glu Lys Gln Ser 340 345 350	1056
aag tca gat cgc aaa aag agc cgc aag gct gag aag aaa gag aag aag Lys Ser Asp Arg Lys Lys Ser Arg Lys Ala Glu Lys Lys Glu Lys Lys 355 360 365	1104
ttc aaa gat tta ttt gtt acc tgg gat cct ccg tct atg gaa atg gat Phe Lys Asp Leu Phe Val Thr Trp Asp Pro Pro Ser Met Glu Met Asp 370 375 380	1152
gat atg gat ctt ggg gac cag gat tgg ctg ctt ggt agt acg agg aaa Asp Met Asp Leu Gly Asp Gln Asp Trp Leu Leu Gly Ser Thr Arg Lys 385 390 395 400	1200

cct gat gct ggc att ggc aac tgc aga gaa att gtt gat cca ctt act 1248
 Pro Asp Ala Gly Ile Gly Asn Cys Arg Glu Ile Val Asp Pro Leu Thr
 405 410 415

tct caa tca gcg gag cag ttc tca ttg cag cct agg gcg att cat tta 1296
 Ser Gln Ser Ala Glu Gln Phe Ser Leu Gln Pro Arg Ala Ile His Leu
 420 425 430

cca gac ctt cat gtc tat cag ttg cca tat gtg gtt cca ttc tag 1341
 Pro Asp Leu His Val Tyr Gln Leu Pro Tyr Val Val Pro Phe
 435 440 445

<210> 16
 <211> 446
 <212> PRT
 <213> Oryza sativa strain IR64

<400> 16

Met Ser Arg Cys Phe Pro Tyr Pro Pro Pro Gly Tyr Val Arg Asn Pro
 1 5 10 15

Val Val Ala Val Ala Ala Ala Glu Ala Gln Ala Thr Thr Lys Leu Gln
 20 25 30

Lys Glu Arg Glu Lys Ala Glu Lys Lys Lys Glu Lys Arg Ser Asp Arg
 35 40 45

Lys Ala Leu Pro His Gly Glu Ile Ser Lys His Ser Lys Arg Thr His
 50 55 60

Lys Lys Arg Lys His Glu Asp Ile Asn Asn Ala Asp Gln Lys Ser Arg
 65 70 75 80

Lys Val Ser Ser Met Glu Pro Gly Glu Gln Leu Glu Lys Ser Gly Leu
 85 90 95

Ser Glu Glu His Gly Ala Pro Cys Phe Thr Gln Thr Val His Gly Ser
 100 105 110

Pro Glu Ser Ser Gln Asp Ser Ser Lys Arg Arg Lys Val Val Leu Pro
 115 120 125

Ser Pro Ser Gln Ala Lys Asn Gly Asn Ile Leu Arg Ile Lys Ile Arg
 130 135 140

Arg Asp Gln Asp Ser Ser Ala Ser Leu Ser Glu Lys Ser Asn Val Val

206720 24064007

145		150		155		160
Gln Thr Pro Val His Gln Met Gly Ser Val Ser Ser Leu Pro Ser Lys	165		170		175	
Lys Asn Ser Met Gln Pro His Asn Thr Glu Met Met Val Arg Thr Ala	180		185		190	
Ser Thr Gln Gln Gln Ser Ile Lys Gly Asp Phe Gln Ala Val Leu Lys	195		200		205	
Gln Gly Met Pro Thr Pro Ala Lys Val Met Pro Arg Val Asp Val Pro	210		215		220	
Pro Ser Met Arg Ala Ser Lys Glu Arg Val Gly Leu Arg Pro Ala Glu	225		230		235	240
Met Leu Ala Asn Val Gly Pro Ser Pro Ser Lys Ala Lys Gln Ile Val	245		250		255	
Asn Pro Ala Ala Ala Lys Val Thr Gln Arg Val Asp Pro Pro Pro Ala	260		265		270	
Lys Ala Ser Gln Arg Ile Asp Pro Leu Leu Pro Ser Lys Val His Ile	275		280		285	
Asp Ala Thr Arg Ser Phe Thr Lys Leu Ser Gln Thr Glu Ile Lys Pro	290		295		300	
Glu Val Gln Pro Pro Ile Pro Lys Val Pro Val Ala Met Pro Thr Ile	305		310		315	320
Asn Arg Gln Gln Ile Asp Thr Ser Gln Pro Lys Glu Glu Pro Cys Ser	325		330		335	
Ser Gly Arg Asn Ala Glu Ala Ala Ser Val Ser Val Glu Lys Gln Ser	340		345		350	
Lys Ser Asp Arg Lys Lys Ser Arg Lys Ala Glu Lys Lys Glu Lys Lys	355		360		365	
Phe Lys Asp Leu Phe Val Thr Trp Asp Pro Pro Ser Met Glu Met Asp	370		375		380	

Asp Met Asp Leu Gly Asp Gln Asp Trp Leu Leu Gly Ser Thr Arg Lys
 385 390 395 400

Pro Asp Ala Gly Ile Gly Asn Cys Arg Glu Ile Val Asp Pro Leu Thr
 405 410 415

Ser Gln Ser Ala Glu Gln Phe Ser Leu Gln Pro Arg Ala Ile His Leu
 420 425 430

Pro Asp Leu His Val Tyr Gln Leu Pro Tyr Val Val Pro Phe
 435 440 445

<210> 17
 <211> 2432
 <212> DNA
 <213> Oryza sativa cv. Kasalath

<220>
 <221> misc_feature
 <222> (1950)..(1950)
 <223> N = G or C

<220>
 <221> misc_feature
 <222> (2032)..(2032)
 <223> N = G or C

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 acgtgccgga tcatttgcgc ttgcctgttg gttttgatcg gatctgttg ttgtgcgtgt 180
 gtgatttggg gatcgacagt ggggggaagc taacctttgc atggataact tgagatttgt 240
 gaggccgcgc ttcgaccaga tcggtcgcca atcttttagt ggctgaccgt ggaaagagga 300
 tattactgac cttcgggtttg ctaatttttg ttgtgccgtt gaatctgaaa taaccagaat 360
 agtcatgggg aaaaaagtct gatctggaag gttcgaatta catttctata tattgttgtg 420
 ctcccagacg atgggttgcaa gaaattactc atgctggata aaattgtgga tgtaagagtc 480
 tgcagttggtt aaaatctgga aacagcacat tttgccgtag taaatttgaa tccatgttgc 540
 tgtctcgtta ttggtgtgtt acgagtaacc tgtgtgttgt tatctccgct tggactagat 600
 tocaagtaat ccagtgccct catgacctgc aaattctatg cctatgaagt aacatgaaca 660

gtttgtatgt attctgttga tgcatacttg cattatattgt gagatgtaca tgttgtggta	720
aaatatttgca ttcaccatat agaaatagta actgactatc cttgttttagt tcgaaaacta	780
ctgcaggttt agttattctc tgttgccaag agtgcttggt atgattgtaa gggttacagt	840
tctgtgacta accatgtaac aaatatatta aggattatca aattattcta tgtgaagtgt	900
ccgtgcccta atttgtttat cttctgtaac tgatagcaca acatttgttt cctgctgtgt	960
gcttgtgtaa attggtactt catcattact atatatattca aagaaaattc tgcattgcat	1020
tcccgtcgtc cgttctaaat cagaactgac gattgctctg gtggctgaag ctccagaaag	1080
aaagggaaaa ggccgaaaag aagaaagaga aaaggagtga caggaaagct cttccacatg	1140
gtgagatatc caagcattca aagcgaaccc acaagaagag aaaacatgaa gacatcaata	1200
atgctgatca gaagtcccgg aaggtttcct ccatggaacc tggtagcaa ttggagaaga	1260
gtggactctc agaagagcat ggagctcctt gctttactca gacagtgcac ggctctccag	1320
agagttcaca ggacagcagc aagagaagaa aggttgtgtt acccagtcct agccaagcta	1380
agaatggtga ggccctttct tgcatttgtc ttcttttagc tggtagatgt gaattggttt	1440
gacttatcct gaattatcat cttgcaggta acatccttcg aataaagata agaagagatc	1500
aagattcttc agcttccctt tcggagaaat ctaatgttgt acaaacacca gttcatcaaa	1560
tgggatcagt ttcatctctg ccaagtaaga aaaactcaat gcaaccacac aacaccgaaa	1620
tgatggtgag aacagcatca acccagcagc aaagcatcaa aggtgatatt caagcagtac	1680
tgaacaagg tatgccaacc ccagcaaaag tcatgccaag agtcgatgtt cctccatcta	1740
tgagggcatc aaaggaaagg gttggccttc gtcctgcaga gatgttggcc aatgttggtc	1800
cttcaccctc caaggcaaaa cagattgtca atcctgcagc tgctaagggt acacaaagag	1860
ttgatcctcc acctgccaaag gcatctcaga gaattgatcc tctgttgcca tccaagggtc	1920
atatagatgc tactcgatct ttacgaagn tctcccagac agagatcaag ccggaagtac	1980
agcccccaat tccgaagggt cctgtggcta tgcctaccat caatcgtcag cngattgaca	2040
cctcgcagcc caaagaagag ccttgctcct ctggcaggaa tgctgaagct gcttcagtat	2100
cagtagagaa gcagtccaag tcagatcgca aaaagagccg caaggctgag aagaaagaga	2160
agaagttcaa agattttatt gttacctggg atcctccgtc tatggaaatg gatgatatgg	2220
atcttgggga ccaggattgg ctgcttggtg gtacgaggaa acctgatgct ggcatggca	2280
actgcagaga aattgttgat ccacttactt ctcaatcagc agagcagttc tcattgcagc	2340

ctagggcgat tcatttacca gaccttcacg tctatcagtt gccatatgtg gttccattct 2400
 aggtttgtgt agtgagatgg agtaggtgag aa 2432

<210> 18
 <211> 1341
 <212> DNA
 <213> Oryza sativa cv. Kasalath

<220>
 <221> CDS
 <222> (1)..(1341)
 <223>

<220>
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 <222> (889)..(889)
 <223> n = G, C

<220>
 <221> misc_feature
 <222> (971)..(971)
 <223> n = A, T

<400> 18
 atg tcg agg tgc ttc ccc tac ccg ccg ccg ggg tac gtg cga aac cca 48
 Met Ser Arg Cys Phe Pro Tyr Pro Pro Pro Gly Tyr Val Arg Asn Pro
 1 5 10 15

gtg gtg gcc gtg gcc gcg gcc gaa gcg cag gcg acc act aag ctc cag 96
 Val Val Ala Val Ala Ala Ala Glu Ala Gln Ala Thr Thr Lys Leu Gln
 20 25 30

aaa gaa agg gaa aag gcc gaa aag aag aaa gag aaa agg agt gac agg 144
 Lys Glu Arg Glu Lys Ala Glu Lys Lys Lys Glu Lys Arg Ser Asp Arg
 35 40 45

aaa gct ctt cca cat ggt gag ata tcc aag cat tca aag cga acc cac 192
 Lys Ala Leu Pro His Gly Glu Ile Ser Lys His Ser Lys Arg Thr His
 50 55 60

aag aag aga aaa cat gaa gac atc aat aat gct gat cag aag tcc cgg 240
 Lys Lys Arg Lys His Glu Asp Ile Asn Asn Ala Asp Gln Lys Ser Arg
 65 70 75 80

aag gtt tcc tcc atg gaa cct ggt gag caa ttg gag aag agt gga ctc 288
 Lys Val Ser Ser Met Glu Pro Gly Glu Gln Leu Glu Lys Ser Gly Leu
 85 90 95

tca gaa gag cat gga gct cct tgc ttt act cag aca gtg cat ggc tct 336
 Ser Glu Glu His Gly Ala Pro Cys Phe Thr Gln Thr Val His Gly Ser
 100 105 110

cca gag agt tca cag gac agc agc aag aga aga aag gtt gtg tta ccc	384
Pro Glu Ser Ser Gln Asp Ser Ser Lys Arg Arg Lys Val Val Leu Pro	
115 120 125	
agt cct agc caa gct aag aat ggt aac atc ctt cga ata aag ata aga	432
Ser Pro Ser Ser Gln Ala Lys Asn Gly Asn Ile Leu Arg Ile Lys Ile Arg	
130 135 140	
aga gat caa gat tct tca gct tcc ctt tcg gag aaa tct aat gtt gta	480
Arg Asp Gln Asp Ser Ser Ala Ser Leu Ser Glu Lys Ser Asn Val Val	
145 150 155 160	
caa aca cca gtt cat caa atg gga tca gtt tca tct ctg cca agt aag	528
Gln Thr Pro Val His Gln Met Gly Ser Val Ser Ser Leu Pro Ser Lys	
165 170 175	
aaa aac tca atg caa cca cac aac acc gaa atg atg gtg aga aca gca	576
Lys Asn Ser Met Gln Pro His Asn Thr Glu Met Met Val Arg Thr Ala	
180 185 190	
tca acc cag cag caa agc atc aaa ggt gat ttt caa gca gta ctg aaa	624
Ser Thr Gln Gln Gln Ser Ile Lys Gly Asp Phe Gln Ala Val Leu Lys	
195 200 205	
caa ggt atg cca acc cca gca aaa gtc atg cca aga gtc gat gtt cct	672
Gln Gly Met Pro Thr Pro Ala Lys Val Met Pro Arg Val Asp Val Pro	
210 215 220	
cca tct atg agg gca tca aag gaa agg gtt ggc ctt cgt cct gca gag	720
Pro Ser Met Arg Ala Ser Lys Glu Arg Val Gly Leu Arg Pro Ala Glu	
225 230 235 240	
atg ttg gcc aat gtt ggt cct tca ccc tcc aag gca aaa cag att gtc	768
Met Leu Ala Asn Val Gly Pro Ser Pro Ser Lys Ala Lys Gln Ile Val	
245 250 255	
aat cct gca gct gct aag gtt aca caa aga gtt gat cct cca cct gcc	816
Asn Pro Ala Ala Ala Lys Val Thr Gln Arg Val Asp Pro Pro Pro Ala	
260 265 270	
aag gca tct cag aga att gat cct ctg ttg cca tcc aag gtt cat ata	864
Lys Ala Ser Gln Arg Ile Asp Pro Leu Leu Pro Ser Lys Val His Ile	
275 280 285	
gat gct act cga tct ttt acg aag ntc tcc cag aca gag atc aag ccg	912
Asp Ala Thr Arg Ser Phe Thr Lys Xaa Ser Gln Thr Glu Ile Lys Pro	
290 295 300	
gaa gta cag ccc cca att ccg aag gtg cct gtg gct atg cct acc atc	960
Glu Val Gln Pro Pro Ile Pro Lys Val Pro Val Ala Met Pro Thr Ile	
305 310 315 320	
aat cgt cag cng att gac acc tcg cag ccc aaa gaa gag cct tgc tcc	1008
Asn Arg Gln Xaa Ile Asp Thr Ser Gln Pro Lys Glu Glu Pro Cys Ser	
325 330 335	
tct ggc agg aat gct gaa gct gct tca gta tca gta gag aag cag tcc	1056

Ser Gly Arg Asn Ala Glu Ala Ala Ser Val Ser Val Glu Lys Gln Ser	
340 345 350	
aag tca gat cgc aaa aag agc cgc aag gct gag aag aaa gag aag aag	1104
Lys Ser Asp Arg Lys Lys Ser Arg Lys Ala Glu Lys Lys Glu Lys Lys	
355 360 365	
ttc aaa gat tta ttt gtt acc tgg gat cct ccg tct atg gaa atg gat	1152
Phe Lys Asp Leu Phe Val Thr Trp Asp Pro Pro Ser Met Glu Met Asp	
370 375 380	
gat atg gat ctt ggg gac cag gat tgg ctg ctt ggt agt acg agg aaa	1200
Asp Met Asp Leu Gly Asp Gln Asp Trp Leu Leu Gly Ser Thr Arg Lys	
385 390 395 400	
cct gat gct ggc att ggc aac tgc aga gaa att gtt gat cca ctt act	1248
Pro Asp Ala Gly Ile Gly Asn Cys Arg Glu Ile Val Asp Pro Leu Thr	
405 410 415	
tct caa tca gca gag cag ttc tca ttg cag cct agg gcg att cat tta	1296
Ser Gln Ser Ala Glu Gln Phe Ser Leu Gln Pro Arg Ala Ile His Leu	
420 425 430	
cca gac ctt cat gtc tat cag ttg cca tat gtg gtt cca ttc tag	1341
Pro Asp Leu His Val Tyr Gln Leu Pro Tyr Val Val Pro Phe	
435 440 445	

<210> 19
 <211> 446
 <212> PRT
 <213> Oryza sativa cv. Kasalath

 <220>
 <221> misc_feature
 <222> (297)..(297)
 <223> The 'Xaa' at location 297 stands for Ile, Val, Leu, or Phe.

 <220>
 <221> misc_feature
 <222> (324)..(324)
 <223> The 'Xaa' at location 324 stands for Gln, Arg, Pro, or Leu.

 <220>
 <221> misc_feature
 <222> (889)..(889)
 <223> n = G, C

 <220>
 <221> misc_feature
 <222> (971)..(971)
 <223> n = A, T

 <400> 19

Met Ser Arg Cys Phe Pro Tyr Pro Pro Pro Gly Tyr Val Arg Asn Pro
1 5 10 15

Val Val Ala Val Ala Ala Ala Glu Ala Gln Ala Thr Thr Lys Leu Gln
20 25 30

Lys Glu Arg Glu Lys Ala Glu Lys Lys Lys Glu Lys Arg Ser Asp Arg
35 40 45

Lys Ala Leu Pro His Gly Glu Ile Ser Lys His Ser Lys Arg Thr His
50 55 60

Lys Lys Arg Lys His Glu Asp Ile Asn Asn Ala Asp Gln Lys Ser Arg
65 70 75 80

Lys Val Ser Ser Met Glu Pro Gly Glu Gln Leu Glu Lys Ser Gly Leu
85 90 95

Ser Glu Glu His Gly Ala Pro Cys Phe Thr Gln Thr Val His Gly Ser
100 105 110

Pro Glu Ser Ser Gln Asp Ser Ser Lys Arg Arg Lys Val Val Leu Pro
115 120 125

Ser Pro Ser Gln Ala Lys Asn Gly Asn Ile Leu Arg Ile Lys Ile Arg
130 135 140

Arg Asp Gln Asp Ser Ser Ala Ser Leu Ser Glu Lys Ser Asn Val Val
145 150 155 160

Gln Thr Pro Val His Gln Met Gly Ser Val Ser Ser Leu Pro Ser Lys
165 170 175

Lys Asn Ser Met Gln Pro His Asn Thr Glu Met Met Val Arg Thr Ala
180 185 190

Ser Thr Gln Gln Gln Ser Ile Lys Gly Asp Phe Gln Ala Val Leu Lys
195 200 205

Gln Gly Met Pro Thr Pro Ala Lys Val Met Pro Arg Val Asp Val Pro
210 215 220

Pro Ser Met Arg Ala Ser Lys Glu Arg Val Gly Leu Arg Pro Ala Glu
225 230 235 240

Met Leu Ala Asn Val Gly Pro Ser Pro Ser Lys Ala Lys Gln Ile Val
 245 250 255

Asn Pro Ala Ala Ala Lys Val Thr Gln Arg Val Asp Pro Pro Pro Ala
 260 265 270

Lys Ala Ser Gln Arg Ile Asp Pro Leu Leu Pro Ser Lys Val His Ile
 275 280 285

Asp Ala Thr Arg Ser Phe Thr Lys Xaa Ser Gln Thr Glu Ile Lys Pro
 290 295 300

Glu Val Gln Pro Pro Ile Pro Lys Val Pro Val Ala Met Pro Thr Ile
 305 310 315 320

Asn Arg Gln Xaa Ile Asp Thr Ser Gln Pro Lys Glu Glu Pro Cys Ser
 325 330 335

Ser Gly Arg Asn Ala Glu Ala Ala Ser Val Ser Val Glu Lys Gln Ser
 340 345 350

Lys Ser Asp Arg Lys Lys Ser Arg Lys Ala Glu Lys Lys Glu Lys Lys
 355 360 365

Phe Lys Asp Leu Phe Val Thr Trp Asp Pro Pro Ser Met Glu Met Asp
 370 375 380

Asp Met Asp Leu Gly Asp Gln Asp Trp Leu Leu Gly Ser Thr Arg Lys
 385 390 395 400

Pro Asp Ala Gly Ile Gly Asn Cys Arg Glu Ile Val Asp Pro Leu Thr
 405 410 415

Ser Gln Ser Ala Glu Gln Phe Ser Leu Gln Pro Arg Ala Ile His Leu
 420 425 430

Pro Asp Leu His Val Tyr Gln Leu Pro Tyr Val Val Pro Phe
 435 440 445

- <210> 20
- <211> 2447
- <212> DNA
- <213> Oryza rufipogon strain 5948

<400> 20
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gctcttgctt gttggttttg atcggatctg ttggttggtg gtgtgtgatt tggggatcgc 180
acgtgcgggg aagctaacct ttgcatggat aacttgagat ttgtgaggcc gcgcttcgac 240
cagatcggtc gccaatcttt tagtggtga ccgtggaaag aggatattac tgaccttcgg 300
tttgctaatt ttggttggtg cgttgaatct gaaataacca gaatagtcac ggggaaaaag 360
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caagaaatta ctcatgctgg ataaaattgt ggatgtaaga gtctgcagtt gttaaaatct 480
ggaaacagca cattttgccg tagtaaattt gaatccatgt tgctgtctcg ttattggtgt 540
gttacgagta acctgtgtgt tgttatctcc gcttgacta gattccaagt aatccagtgc 600
cttcatgacc tgcaaattct atgcctatga agtaacatga acagtttgta tgtattctgt 660
tgatgcatac ttgcattatt tgtgagatgt acatgttggt gtaaaatttt gcattcacca 720
tatagaaata gtaattgact atccttggtt agttcgaaaa cttctgcagg tttagttatt 780
ctctgttgcc aagagtgcct gttatgattg taagggttac agttctgtga ctaaccatgt 840
aacaatatata ttaaggatta tcaaattatt ctatgtgaag tgtccgtgcc ctaattgtgt 900
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206120"24064001

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gatccactta cttctcaatc agcggagcag ttctcattgc agcctagggc gattcattta 2340
ccagaccttc atgtctatca gttgccatat gtgggtccat tctaggtttg tgtagtgaga 2400
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<210> 21
<211> 1341
<212> DNA
<213> Oryza rufipogon strain 5948

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<220>
<221> CDS
<222> (1)..(1341)
<223>

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<220>
<221> misc_feature
<222> (1)..(15)
<223> n = A, C, G, T

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Xaa Xaa Xaa Xaa Xaa Pro Tyr Pro Pro Pro Gly Tyr Val Arg Asn Pro
1 5 10 15

gtg gtg gcc gtg gcc gcg gcc gaa gcg cag gcg acc act aag ctc cag 96
Val Val Ala Val Ala Ala Ala Glu Ala Gln Ala Thr Thr Lys Leu Gln
20 25 30

aaa gaa agg gaa aag gcc gaa aag aag aaa gag aaa agg agt gac agg 144
Lys Glu Arg Glu Lys Ala Glu Lys Lys Lys Glu Lys Arg Ser Asp Arg
35 40 45

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aaa gct ctt cca cat ggt gag ata tcc aag cat tca aag cga acc cac Lys Ala Leu Pro His Gly Glu Ile Ser Lys His Ser Lys Arg Thr His 50 55 60	192
aag aag aga aaa cat gaa gac atc aat aat gct gat cag aag tcc cgg Lys Lys Arg Lys His Glu Asp Ile Asn Asn Ala Asp Gln Lys Ser Arg 65 70 75 80	240
aag gtt tcc tcc atg gaa cct ggt gag caa ttg gag aag agt gga ctc Lys Val Ser Ser Met Glu Pro Gly Glu Gln Leu Glu Lys Ser Gly Leu 85 90 95	288
tca gaa gag cat gga gct cct tgc ttt act cag aca gtg cat ggc tct Ser Glu Glu His Gly Ala Pro Cys Phe Thr Gln Thr Val His Gly Ser 100 105 110	336
cca gag agt tca cag gac agc agc aag aga aga aag gtt gtg tta ccc Pro Glu Ser Ser Gln Asp Ser Ser Lys Arg Arg Lys Val Val Leu Pro 115 120 125	384
agt cct agc caa gct aag aat ggt aac atc ctt cga ata aag ata aga Ser Pro Ser Gln Ala Lys Asn Gly Asn Ile Leu Arg Ile Lys Ile Arg 130 135 140	432
aga gat caa gat tct tca gct tcc ctt tcg gag aaa tct aat gtt gta Arg Asp Gln Asp Ser Ser Ala Ser Leu Ser Glu Lys Ser Asn Val Val 145 150 155 160	480
caa aca cca gtt cat caa atg gga tca gtt tca tct ctg cca agt aag Gln Thr Pro Val His Gln Met Gly Ser Val Ser Ser Leu Pro Ser Lys 165 170 175	528
aaa aac tca atg caa cca cac aac acc gaa atg atg gtg aga aca gca Lys Asn Ser Met Gln Pro His Asn Thr Glu Met Met Val Arg Thr Ala 180 185 190	576
tca acc cag cag caa agc atc aaa ggt gat ttt caa gca gta ctg aaa Ser Thr Gln Gln Gln Ser Ile Lys Gly Asp Phe Gln Ala Val Leu Lys 195 200 205	624
caa ggt atg cca acc cca gca aaa gtc atg cca aga gtc gat gtt cct Gln Gly Met Pro Thr Pro Ala Lys Val Met Pro Arg Val Asp Val Pro 210 215 220	672
cca tct atg agg gca tca aag gaa agg gtt ggc ctt cgt cct gca gag Pro Ser Met Arg Ala Ser Lys Glu Arg Val Gly Leu Arg Pro Ala Glu 225 230 235 240	720
atg ttg gcc aat gtt ggt cct tca ccc tcc aag gca aaa cag att gtc Met Leu Ala Asn Val Gly Pro Ser Pro Ser Lys Ala Lys Gln Ile Val 245 250 255	768
aat cct gca gct gct aag gtt aca caa aga gtt gat cct cca cct gcc Asn Pro Ala Ala Ala Lys Val Thr Gln Arg Val Asp Pro Pro Pro Ala 260 265 270	816

aag gca tct cag aga att gat cct ctg ttg cca tcc aag gtt cat ata	864
Lys Ala Ser Gln Arg Ile Asp Pro Leu Leu Pro Ser Lys Val His Ile	
275 280 285	
gat gct act cga tct ttt acg aag ctc tcc cag aca gag atc aag ccg	912
Asp Ala Thr Arg Ser Phe Thr Lys Leu Ser Gln Thr Glu Ile Lys Pro	
290 295 300	
gaa gta cag ccc cca att ccg aag gtg cct gtg gct atg cct acc atc	960
Glu Val Gln Pro Pro Ile Pro Lys Val Pro Val Ala Met Pro Thr Ile	
305 310 315 320	
aat cgt cag cag att gac acc tcg cag ccc aaa gaa gag cct tgc tcc	1008
Asn Arg Gln Gln Ile Asp Thr Ser Gln Pro Lys Glu Glu Pro Cys Ser	
325 330 335	
tct ggc agg aat gct gaa gct gct tca gta tca gta gag aag cag tcc	1056
Ser Gly Arg Asn Ala Glu Ala Ala Ser Val Ser Val Glu Lys Gln Ser	
340 345 350	
aag tca gat cgc aaa aag agc cgc aag gct gag aag aaa gag aag aag	1104
Lys Ser Asp Arg Lys Lys Ser Arg Lys Ala Glu Lys Lys Glu Lys Lys	
355 360 365	
ttc aaa gat tta ttt gtt acc tgg gat cct ccg tct atg gaa atg gat	1152
Phe Lys Asp Leu Phe Val Thr Trp Asp Pro Pro Ser Met Glu Met Asp	
370 375 380	
gat atg gat ctt ggg gac cag gat tgg ctg ctt ggt agt acg agg aaa	1200
Asp Met Asp Leu Gly Asp Gln Asp Trp Leu Leu Gly Ser Thr Arg Lys	
385 390 395 400	
cct gat gct ggc att ggc aac tgc aga gaa att gtt gat cca ctt act	1248
Pro Asp Ala Gly Ile Gly Asn Cys Arg Glu Ile Val Asp Pro Leu Thr	
405 410 415	
tct caa tca gcg gag cag ttc tca ttg cag cct agg gcg att cat tta	1296
Ser Gln Ser Ala Glu Gln Phe Ser Leu Gln Pro Arg Ala Ile His Leu	
420 425 430	
cca gac ctt cat gtc tat cag ttg cca tat gtg gtt cca ttc tag	1341
Pro Asp Leu His Val Tyr Gln Leu Pro Tyr Val Val Pro Phe	
435 440 445	

<210> 22
 <211> 446
 <212> PRT
 <213> Oryza rufipogon strain 5948

<220>
 <221> misc_feature
 <222> (1)..(1)
 <223> The 'Xaa' at location 1 stands for Lys, Asn, Arg, Ser, Thr, Ile, Met, Glu, Asp, Gly, Ala, Val, Gln, His, Pro, Leu, a stop codon, Tyr, Trp, Cys, or Phe.

205120 2406400

<220>
<221> misc_feature
<222> (2)..(2)
<223> The 'Xaa' at location 2 stands for Lys, Asn, Arg, Ser, Thr, Ile, Met, Glu, Asp, Gly, Ala, Val, Gln, His, Pro, Leu, a stop codon, Tyr, Trp, Cys, or Phe.

<220>
<221> misc_feature
<222> (3)..(3)
<223> The 'Xaa' at location 3 stands for Lys, Asn, Arg, Ser, Thr, Ile, Met, Glu, Asp, Gly, Ala, Val, Gln, His, Pro, Leu, a stop codon, Tyr, Trp, Cys, or Phe.

<220>
<221> misc_feature
<222> (4)..(4)
<223> The 'Xaa' at location 4 stands for Lys, Asn, Arg, Ser, Thr, Ile, Met, Glu, Asp, Gly, Ala, Val, Gln, His, Pro, Leu, a stop codon, Tyr, Trp, Cys, or Phe.

<220>
<221> misc_feature
<222> (5)..(5)
<223> The 'Xaa' at location 5 stands for Lys, Asn, Arg, Ser, Thr, Ile, Met, Glu, Asp, Gly, Ala, Val, Gln, His, Pro, Leu, a stop codon, Tyr, Trp, Cys, or Phe.

<220>
<221> misc_feature
<222> (1)..(15)
<223> n = A, C, G, T

<400> 22

Xaa Xaa Xaa Xaa Xaa Pro Tyr Pro Pro Pro Gly Tyr Val Arg Asn Pro
1 5 10 15

Val Val Ala Val Ala Ala Ala Glu Ala Gln Ala Thr Thr Lys Leu Gln
20 25 30

Lys Glu Arg Glu Lys Ala Glu Lys Lys Lys Glu Lys Arg Ser Asp Arg
35 40 45

Lys Ala Leu Pro His Gly Glu Ile Ser Lys His Ser Lys Arg Thr His
50 55 60

Lys Lys Arg Lys His Glu Asp Ile Asn Asn Ala Asp Gln Lys Ser Arg
65 70 75 80

Lys Val Ser Ser Met Glu Pro Gly Glu Gln Leu Glu Lys Ser Gly Leu
85 90 95

Ser Glu Glu His Gly Ala Pro Cys Phe Thr Gln Thr Val His Gly Ser
100 105 110

Pro Glu Ser Ser Gln Asp Ser Ser Lys Arg Arg Lys Val Val Leu Pro
115 120 125

Ser Pro Ser Gln Ala Lys Asn Gly Asn Ile Leu Arg Ile Lys Ile Arg
130 135 140

Arg Asp Gln Asp Ser Ser Ala Ser Leu Ser Glu Lys Ser Asn Val Val
145 150 155 160

Gln Thr Pro Val His Gln Met Gly Ser Val Ser Ser Leu Pro Ser Lys
165 170 175

Lys Asn Ser Met Gln Pro His Asn Thr Glu Met Met Val Arg Thr Ala
180 185 190

Ser Thr Gln Gln Gln Ser Ile Lys Gly Asp Phe Gln Ala Val Leu Lys
195 200 205

Gln Gly Met Pro Thr Pro Ala Lys Val Met Pro Arg Val Asp Val Pro
210 215 220

Pro Ser Met Arg Ala Ser Lys Glu Arg Val Gly Leu Arg Pro Ala Glu
225 230 235 240

Met Leu Ala Asn Val Gly Pro Ser Pro Ser Lys Ala Lys Gln Ile Val
245 250 255

Asn Pro Ala Ala Ala Lys Val Thr Gln Arg Val Asp Pro Pro Pro Ala
260 265 270

Lys Ala Ser Gln Arg Ile Asp Pro Leu Leu Pro Ser Lys Val His Ile
275 280 285

Asp Ala Thr Arg Ser Phe Thr Lys Leu Ser Gln Thr Glu Ile Lys Pro
290 295 300

Glu Val Gln Pro Pro Ile Pro Lys Val Pro Val Ala Met Pro Thr Ile
305 310 315 320

206120" 2406200T

Asn Arg Gln Gln Ile Asp Thr Ser Gln Pro Lys Glu Glu Pro Cys Ser
325 330 335

Ser Gly Arg Asn Ala Glu Ala Ala Ser Val Ser Val Glu Lys Gln Ser
340 345 350

Lys Ser Asp Arg Lys Lys Ser Arg Lys Ala Glu Lys Lys Glu Lys Lys
355 360 365

Phe Lys Asp Leu Phe Val Thr Trp Asp Pro Pro Ser Met Glu Met Asp
370 375 380

Asp Met Asp Leu Gly Asp Gln Asp Trp Leu Leu Gly Ser Thr Arg Lys
385 390 395 400

Pro Asp Ala Gly Ile Gly Asn Cys Arg Glu Ile Val Asp Pro Leu Thr
405 410 415

Ser Gln Ser Ala Glu Gln Phe Ser Leu Gln Pro Arg Ala Ile His Leu
420 425 430

Pro Asp Leu His Val Tyr Gln Leu Pro Tyr Val Val Pro Phe
435 440 445

<210> 23
<211> 146
<212> DNA
<213> Oryza rufipogon strain 5949

<400> 23
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cgaggtgctt cccctacccg ccgccgggggt acgtgcgaaa ccagtggtg gccgtggccg 120
cggccgaagc gcaggcgacc actaag 146

<210> 24
<211> 1615
<212> DNA
<213> Oryza rufipogon strain 5949

<400> 24
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ccgtgcccta attgtgttat cttctgtaac tgatagcaca acatttggtt cctgctgtgt 120
gcttgtgtaa attggtactt catcattact atatatttca aagaaaattc tgcattgcat 180

tcccgtcgtc cgttctaaat cagaactgac gattgctctg gtggctgaag ctccagaaag	240
aaagggaaaa ggccgaaaag aagaaagaga aaaagagtga caggaaagct cttccacatg	300
gtgagatata caagcattca aagcgaaccc acaagaagag aaaacatgaa gacatcaata	360
atgctgatca gaagtcccg aaggtttcct ccatggaacc tggtagcaa ttggagaaga	420
gtggactctc agaagagcat ggagctcctt gctttactca gacagtgcac ggctctccag	480
agagttcaca ggacagcagc aagagaagaa aggttgtgtt acccagtcct agccaagcta	540
agaatggtga ggccctttct tgcatttgtc ttctcttagc tggtagatgtt gaattggttt	600
gacttatcct gaattatcat cttgcaggta acatccttcg aataaagata agaagagatc	660
aagattcttc agcttccctt tcggagaaat ctaatgttgt acaaacacca gttcatcaaa	720
tgggatcagt ttcattctctg ccaagtaaga aaaactcaat gcaaccacac aacaccgaaa	780
tgatggtgag aacagcatca acccagcagc aaagcatcaa aggtgatgtt caagcagtag	840
tgaacaagg tatgccaacc ccagcaaaag tcatgccaag agtcgatgtt cctccatcta	900
tgagggcatc aaaggaaagg gttggccttc gtccctgcaga gatgttggtc aatgttggtc	960
cttcaccatc caaggcaaaa cagattgtca atcctgcagc tgctaagggtt acacaaagag	1020
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atatagatgc tactcgatct ttacgaagg tctccagac agagatcaag ccggaagtac	1140
agccccaat tccgaagggtg cctgtggcta tgcctaccat caatcgtag cagattgaca	1200
cctgcagacc caaagaagag ccttgctcct ctggcaggaa tgctgaagct gcttcagtat	1260
cagtagagaa gcagtccaag tcagatcgca aaaagagccg caaggctgag aagaaagaga	1320
agaagttcaa agatttattt gttacctggg atcctccgtc tatggaaatg gatgatatgg	1380
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actgcagaga aattgttgat ccacttactt ctcaatcagc agagcagttc tcattgcagc	1500
ctagggcgat tcatttacca gaccttcag tctatcagtt gccatatgtg gttccattct	1560
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<210> 25
 <211> 1341
 <212> DNA
 <213> Oryza rufipogon strain 5949

<220>
 <221> CDS

<222> (1)..(1341)

<223>

<400> 25

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gtg gtg gcc gtg gcc gcg gcc gaa gcg cag gcg acc act aag ctc cag	96
Val Val Ala Val Ala Ala Ala Glu Ala Gln Ala Thr Thr Lys Leu Gln	
20 25 30	
aaa gaa agg gaa aag gcc gaa aag aag aaa gag aaa aag agt gac agg	144
Lys Glu Arg Glu Lys Ala Glu Lys Lys Lys Glu Lys Lys Ser Asp Arg	
35 40 45	
aaa gct ctt cca cat ggt gag ata tcc aag cat tca aag cga acc cac	192
Lys Ala Leu Pro His Gly Glu Ile Ser Lys His Ser Lys Arg Thr His	
50 55 60	
aag aag aga aaa cat gaa gac atc aat aat gct gat cag aag tcc cgg	240
Lys Lys Arg Lys His Glu Asp Ile Asn Asn Ala Asp Gln Lys Ser Arg	
65 70 75 80	
aag gtt tcc tcc atg gaa cct ggt gag caa ttg gag aag agt gga ctc	288
Lys Val Ser Ser Met Glu Pro Gly Glu Gln Leu Glu Lys Ser Gly Leu	
85 90 95	
tca gaa gag cat gga gct cct tgc ttt act cag aca gtg cat ggc tct	336
Ser Glu Glu His Gly Ala Pro Cys Phe Thr Gln Thr Val His Gly Ser	
100 105 110	
cca gag agt tca cag gac agc agc aag aga aga aag gtt gtg tta ccc	384
Pro Glu Ser Ser Gln Asp Ser Ser Lys Arg Arg Lys Val Val Leu Pro	
115 120 125	
agt cct agc caa gct aag aat ggt aac atc ctt cga ata aag ata aga	432
Ser Pro Ser Gln Ala Lys Asn Gly Asn Ile Leu Arg Ile Lys Ile Arg	
130 135 140	
aga gat caa gat tct tca gct tcc ctt tcg gag aaa tct aat gtt gta	480
Arg Asp Gln Asp Ser Ser Ala Ser Leu Ser Glu Lys Ser Asn Val Val	
145 150 155 160	
caa aca cca gtt cat caa atg gga tca gtt tca tct ctg cca agt aag	528
Gln Thr Pro Val His Gln Met Gly Ser Val Ser Ser Leu Pro Ser Lys	
165 170 175	
aaa aac tca atg caa cca cac aac acc gaa atg atg gtg aga aca gca	576
Lys Asn Ser Met Gln Pro His Asn Thr Glu Met Met Val Arg Thr Ala	
180 185 190	
tca acc cag cag caa agc atc aaa ggt gat ttt caa gca gta ctg aaa	624
Ser Thr Gln Gln Gln Ser Ile Lys Gly Asp Phe Gln Ala Val Leu Lys	
195 200 205	

caa ggt atg cca acc cca gca aaa gtc atg cca aga gtc gat gtt cct Gln Gly Met Pro Thr Pro Ala Lys Val Met Pro Arg Val Asp Val Pro 210 215 220	672
cca tct atg agg gca tca aag gaa agg gtt ggc ctt cgt cct gca gag Pro Ser Met Arg Ala Ser Lys Glu Arg Val Gly Leu Arg Pro Ala Glu 225 230 235 240	720
atg ttg gcc aat gtt ggt cct tca cca tcc aag gca aaa cag att gtc Met Leu Ala Asn Val Gly Pro Ser Pro Ser Lys Ala Lys Gln Ile Val 245 250 255	768
aat cct gca gct gct aag gtt aca caa aga gtt gat cct cca cct gcc Asn Pro Ala Ala Ala Lys Val Thr Gln Arg Val Asp Pro Pro Pro Ala 260 265 270	816
aag gca tct cag aga att gat cct ctg ttg cca tcc aag gtt cat ata Lys Ala Ser Gln Arg Ile Asp Pro Leu Leu Pro Ser Lys Val His Ile 275 280 285	864
gat gct act cga tct ttt acg aag gtc tcc cag aca gag atc aag ccg Asp Ala Thr Arg Ser Phe Thr Lys Val Ser Gln Thr Glu Ile Lys Pro 290 295 300	912
gaa gta cag ccc cca att ccg aag gtg cct gtg gct atg cct acc atc Glu Val Gln Pro Pro Ile Pro Lys Val Pro Val Ala Met Pro Thr Ile 305 310 315 320	960
aat cgt cag cag att gac acc tcg cag ccc aaa gaa gag cct tgc tcc Asn Arg Gln Gln Ile Asp Thr Ser Gln Pro Lys Glu Glu Pro Cys Ser 325 330 335	1008
tct ggc agg aat gct gaa gct gct tca gta tca gta gag aag cag tcc Ser Gly Arg Asn Ala Glu Ala Ala Ser Val Ser Val Glu Lys Gln Ser 340 345 350	1056
aag tca gat cgc aaa aag agc cgc aag gct gag aag aaa gag aag aag Lys Ser Asp Arg Lys Lys Ser Arg Lys Ala Glu Lys Lys Glu Lys Lys 355 360 365	1104
ttc aaa gat tta ttt gtt acc tgg gat cct ccg tct atg gaa atg gat Phe Lys Asp Leu Phe Val Thr Trp Asp Pro Pro Ser Met Glu Met Asp 370 375 380	1152
gat atg gat ctt ggg gac cag gat tgg ctg ctt ggt agt acg agg aaa Asp Met Asp Leu Gly Asp Gln Asp Trp Leu Leu Gly Ser Thr Arg Lys 385 390 395 400	1200
cct gat gct ggc att ggc aac tgc aga gaa att gtt gat cca ctt act Pro Asp Ala Gly Ile Gly Asn Cys Arg Glu Ile Val Asp Pro Leu Thr 405 410 415	1248
tct caa tca gca gag cag ttc tca ttg cag cct agg gcg att cat tta Ser Gln Ser Ala Glu Gln Phe Ser Leu Gln Pro Arg Ala Ile His Leu 420 425 430	1296
cca gac ctt cat gtc tat cag ttg cca tat gtg gtt cca ttc tag	1341

Pro Asp Leu His Val Tyr Gln Leu Pro Tyr Val Val Pro Phe
 435 440 445

<210> 26
 <211> 446
 <212> PRT
 <213> Oryza rufipogon strain 5949

<400> 26

Met Ser Arg Cys Phe Pro Tyr Pro Pro Pro Gly Tyr Val Arg Asn Pro
 1 5 10 15

Val Val Ala Val Ala Ala Ala Glu Ala Gln Ala Thr Thr Lys Leu Gln
 20 25 30

Lys Glu Arg Glu Lys Ala Glu Lys Lys Lys Glu Lys Lys Ser Asp Arg
 35 40 45

Lys Ala Leu Pro His Gly Glu Ile Ser Lys His Ser Lys Arg Thr His
 50 55 60

Lys Lys Arg Lys His Glu Asp Ile Asn Asn Ala Asp Gln Lys Ser Arg
 65 70 75 80

Lys Val Ser Ser Met Glu Pro Gly Glu Gln Leu Glu Lys Ser Gly Leu
 85 90 95

Ser Glu Glu His Gly Ala Pro Cys Phe Thr Gln Thr Val His Gly Ser
 100 105 110

Pro Glu Ser Ser Gln Asp Ser Ser Lys Arg Arg Lys Val Val Leu Pro
 115 120 125

Ser Pro Ser Gln Ala Lys Asn Gly Asn Ile Leu Arg Ile Lys Ile Arg
 130 135 140

Arg Asp Gln Asp Ser Ser Ala Ser Leu Ser Glu Lys Ser Asn Val Val
 145 150 155 160

Gln Thr Pro Val His Gln Met Gly Ser Val Ser Ser Leu Pro Ser Lys
 165 170 175

Lys Asn Ser Met Gln Pro His Asn Thr Glu Met Met Val Arg Thr Ala
 180 185 190

Ser Thr Gln Gln Gln Ser Ile Lys Gly Asp Phe Gln Ala Val Leu Lys
195 200 205

Gln Gly Met Pro Thr Pro Ala Lys Val Met Pro Arg Val Asp Val Pro
210 215 220

Pro Ser Met Arg Ala Ser Lys Glu Arg Val Gly Leu Arg Pro Ala Glu
225 230 235 240

Met Leu Ala Asn Val Gly Pro Ser Pro Ser Lys Ala Lys Gln Ile Val
245 250 255

Asn Pro Ala Ala Ala Lys Val Thr Gln Arg Val Asp Pro Pro Pro Ala
260 265 270

Lys Ala Ser Gln Arg Ile Asp Pro Leu Leu Pro Ser Lys Val His Ile
275 280 285

Asp Ala Thr Arg Ser Phe Thr Lys Val Ser Gln Thr Glu Ile Lys Pro
290 295 300

Glu Val Gln Pro Pro Ile Pro Lys Val Pro Val Ala Met Pro Thr Ile
305 310 315 320

Asn Arg Gln Gln Ile Asp Thr Ser Gln Pro Lys Glu Glu Pro Cys Ser
325 330 335

Ser Gly Arg Asn Ala Glu Ala Ala Ser Val Ser Val Glu Lys Gln Ser
340 345 350

Lys Ser Asp Arg Lys Lys Ser Arg Lys Ala Glu Lys Lys Glu Lys Lys
355 360 365

Phe Lys Asp Leu Phe Val Thr Trp Asp Pro Pro Ser Met Glu Met Asp
370 375 380

Asp Met Asp Leu Gly Asp Gln Asp Trp Leu Leu Gly Ser Thr Arg Lys
385 390 395 400

Pro Asp Ala Gly Ile Gly Asn Cys Arg Glu Ile Val Asp Pro Leu Thr
405 410 415

Ser Gln Ser Ala Glu Gln Phe Ser Leu Gln Pro Arg Ala Ile His Leu
 420 425 430

Pro Asp Leu His Val Tyr Gln Leu Pro Tyr Val Val Pro Phe
 435 440 445

<210> 27
 <211> 107
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 <213> Oryza rufipogon strain 5953

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<210> 28
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 gacatcaata atgctgatca gaagtcccg aaggtttcct ccatggaacc tggtagcaa 180
 ttggagaaga gtggactctc agaagagcat ggagctcctt gctttactca gacagtgcac 240
 ggctctccag agagttcaca ggacagcagc aagagaagaa aggttgtgtt acccagtcct 300
 agccaagcta agaattgtga ggccctttct tgcatttttc ttcttttagc tggtagtgtt 360
 gaattgggtt gacttatcct gaattatcat cttgcaggta acatccttcg aataaagata 420
 agaagagatc aagattcttc agcttccctt tcggagaaat ctaattgtgt acaaacacca 480
 gttcatcaaa tgggatcagt ttcattctctg ccaagtaaga aaaactcaat gcaaccacac 540
 aacaccgaaa tgatggtgag aacagcatca acccagcagc aaagcatcaa aggtgatttt 600
 caagcagtac tgaaacaagg tatgccaacc ccagcaaaag tcatgccaag agtcgatgtt 660
 cctccatcta tgagggcatc aaaggaaagg gttggccttc gtctgcaga gatgttggcc 720
 aatgttggtc cttaccctc caaggcaaaa cagattgtca atcctgcagc tgctaagggtt 780
 acacaaagag ttgatcctcc acctgccaag gcattctcaga gaattgatcc tctgttgcca 840
 tccaagggtc atatagatgc tactcgatct ttacgaagc tctcccagac agagatcaag 900
 ccggaagtac agccccaat tccgaagggtg cctgtggcta tgcctaccat caatcgtag 960

cagattgaca cctcgcagcc caaagaagag ccttgctcct ctggcaggaa tgctgaagct 1020
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aagaaagaga agaagttcaa agattttatgt gttacctggg atcctccgtc tatggaaatg 1140
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Val Val Ala Val Ala Ala Ala Glu Ala Gln Ala Thr Thr Lys Leu Gln
20 25 30
aaa gaa agg gaa aag gcc gaa aag aag aaa gag aaa aag agt gac agg 144
Lys Glu Arg Glu Lys Ala Glu Lys Lys Lys Glu Lys Lys Ser Asp Arg
35 40 45
aaa gct ctt cca cat ggt gag ata tcc aag cat tca aag cga acc cac 192
Lys Ala Leu Pro His Gly Glu Ile Ser Lys His Ser Lys Arg Thr His
50 55 60
aag aag aga aaa cat gaa gac atc aat aat gct gat cag aag tcc cgg 240
Lys Lys Arg Lys His Glu Asp Ile Asn Asn Ala Asp Gln Lys Ser Arg
65 70 75 80
aag gtt tcc tcc atg gaa cct ggt gag caa ttg gag aag agt gga ctc 288
Lys Val Ser Ser Met Glu Pro Gly Glu Gln Leu Glu Lys Ser Gly Leu
85 90 95
tca gaa gag cat gga gct cct tgc ttt act cag aca gtg cat ggc tct 336
Ser Glu Glu His Gly Ala Pro Cys Phe Thr Gln Thr Val His Gly Ser
100 105 110
cca gag agt tca cag gac agc agc aag aga aga aag gtt gtg tta ccc 384

Pro Glu Ser Ser Gln Asp Ser Ser Lys Arg Arg Lys Val Val Leu Pro	
115 120 125	
agt cct agc caa gct aag aat ggt aac atc ctt cga ata aag ata aga	432
Ser Pro Ser Gln Ala Lys Asn Gly Asn Ile Leu Arg Ile Lys Ile Arg	
130 135 140	
aga gat caa gat tct tca gct tcc ctt tcg gag aaa tct aat gtt gta	480
Arg Asp Gln Asp Ser Ser Ala Ser Leu Ser Glu Lys Ser Asn Val Val	
145 150 155 160	
caa aca cca gtt cat caa atg gga tca gtt tca tct ctg cca agt aag	528
Gln Thr Pro Val His Gln Met Gly Ser Val Ser Ser Leu Pro Ser Lys	
165 170 175	
aaa aac tca atg caa cca cac aac acc gaa atg atg gtg aga aca gca	576
Lys Asn Ser Met Gln Pro His Asn Thr Glu Met Met Val Arg Thr Ala	
180 185 190	
tca acc cag cag caa agc atc aaa ggt gat ttt caa gca gta ctg aaa	624
Ser Thr Gln Gln Gln Ser Ile Lys Gly Asp Phe Gln Ala Val Leu Lys	
195 200 205	
caa ggt atg cca acc cca gca aaa gtc atg cca aga gtc gat gtt cct	672
Gln Gly Met Pro Thr Pro Ala Lys Val Met Pro Arg Val Asp Val Pro	
210 215 220	
cca tct atg agg gca tca aag gaa agg gtt ggc ctt cgt cct gca gag	720
Pro Ser Met Arg Ala Ser Lys Glu Arg Val Gly Leu Arg Pro Ala Glu	
225 230 235 240	
atg ttg gcc aat gtt ggt cct tca ccc tcc aag gca aaa cag att gtc	768
Met Leu Ala Asn Val Gly Pro Ser Pro Ser Lys Ala Lys Gln Ile Val	
245 250 255	
aat cct gca gct gct aag gtt aca caa aga gtt gat cct cca cct gcc	816
Asn Pro Ala Ala Ala Lys Val Thr Gln Arg Val Asp Pro Pro Pro Ala	
260 265 270	
aag gca tct cag aga att gat cct ctg ttg cca tcc aag gtt cat ata	864
Lys Ala Ser Gln Arg Ile Asp Pro Leu Leu Pro Ser Lys Val His Ile	
275 280 285	
gat gct act cga tct ttt acg aag ctc tcc cag aca gag atc aag ccg	912
Asp Ala Thr Arg Ser Phe Thr Lys Leu Ser Gln Thr Glu Ile Lys Pro	
290 295 300	
gaa gta cag ccc cca att ccg aag gtg cct gtg gct atg cct acc atc	960
Glu Val Gln Pro Pro Ile Pro Lys Val Pro Val Ala Met Pro Thr Ile	
305 310 315 320	
aat cgt cag cag att gac acc tcg cag ccc aaa gaa gag cct tgc tcc	1008
Asn Arg Gln Gln Ile Asp Thr Ser Gln Pro Lys Glu Glu Pro Cys Ser	
325 330 335	
tct ggc agg aat gct gaa gct gct tca gta tca gta gag aag cag tcc	1056
Ser Gly Arg Asn Ala Glu Ala Ala Ser Val Ser Val Glu Lys Gln Ser	

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340	345	350	
aag tca gat cgc aaa aag agc cgc aag gct gag aag aaa gag aag aag Lys Ser Asp Arg Lys Lys Ser Arg Lys Ala Glu Lys Lys Glu Lys Lys 355 360 365			1104
ttc aaa gat tta ttt gtt acc tgg gat cct ccg tct atg gaa atg gat Phe Lys Asp Leu Phe Val Thr Trp Asp Pro Pro Ser Met Glu Met Asp 370 375 380			1152
gat atg gat ctt ggg gac cag gat tgg ctg ctt ggt agt acg agg aaa Asp Met Asp Leu Gly Asp Gln Asp Trp Leu Leu Gly Ser Thr Arg Lys 385 390 395 400			1200
cct gat gct ggc att ggc aac tgc aga gaa att gtt gat cca ctt act Pro Asp Ala Gly Ile Gly Asn Cys Arg Glu Ile Val Asp Pro Leu Thr 405 410 415			1248
tct caa tca gcg gag cag ttc tca ttg cag cct agg gcg att cat tta Ser Gln Ser Ala Glu Gln Phe Ser Leu Gln Pro Arg Ala Ile His Leu 420 425 430			1296
cca gac ctt cat gtc tat cag ttg cca tat gtg gtt cca ttc tag Pro Asp Leu His Val Tyr Gln Leu Pro Tyr Val Val Pro Phe 435 440 445			1341
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Lys Glu Arg Glu Lys Ala Glu Lys Lys Lys Glu Lys Lys Ser Asp Arg 35 40 45			
Lys Ala Leu Pro His Gly Glu Ile Ser Lys His Ser Lys Arg Thr His 50 55 60			
Lys Lys Arg Lys His Glu Asp Ile Asn Asn Ala Asp Gln Lys Ser Arg 65 70 75 80			
Lys Val Ser Ser Met Glu Pro Gly Glu Gln Leu Glu Lys Ser Gly Leu 85 90 95			

Ser Glu Glu His Gly Ala Pro Cys Phe Thr Gln Thr Val His Gly Ser
100 105 110

Pro Glu Ser Ser Gln Asp Ser Ser Lys Arg Arg Lys Val Val Leu Pro
115 120 125

Ser Pro Ser Gln Ala Lys Asn Gly Asn Ile Leu Arg Ile Lys Ile Arg
130 135 140

Arg Asp Gln Asp Ser Ser Ala Ser Leu Ser Glu Lys Ser Asn Val Val
145 150 155 160

Gln Thr Pro Val His Gln Met Gly Ser Val Ser Ser Leu Pro Ser Lys
165 170 175

Lys Asn Ser Met Gln Pro His Asn Thr Glu Met Met Val Arg Thr Ala
180 185 190

Ser Thr Gln Gln Gln Ser Ile Lys Gly Asp Phe Gln Ala Val Leu Lys
195 200 205

Gln Gly Met Pro Thr Pro Ala Lys Val Met Pro Arg Val Asp Val Pro
210 215 220

Pro Ser Met Arg Ala Ser Lys Glu Arg Val Gly Leu Arg Pro Ala Glu
225 230 235 240

Met Leu Ala Asn Val Gly Pro Ser Pro Ser Lys Ala Lys Gln Ile Val
245 250 255

Asn Pro Ala Ala Ala Lys Val Thr Gln Arg Val Asp Pro Pro Pro Ala
260 265 270

Lys Ala Ser Gln Arg Ile Asp Pro Leu Leu Pro Ser Lys Val His Ile
275 280 285

Asp Ala Thr Arg Ser Phe Thr Lys Leu Ser Gln Thr Glu Ile Lys Pro
290 295 300

Glu Val Gln Pro Pro Ile Pro Lys Val Pro Val Ala Met Pro Thr Ile
305 310 315 320

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Asn Arg Gln Gln Ile Asp Thr Ser Gln Pro Lys Glu Glu Pro Cys Ser
325 330 335

Ser Gly Arg Asn Ala Glu Ala Ala Ser Val Ser Val Glu Lys Gln Ser
340 345 350

Lys Ser Asp Arg Lys Lys Ser Arg Lys Ala Glu Lys Lys Glu Lys Lys
355 360 365

Phe Lys Asp Leu Phe Val Thr Trp Asp Pro Pro Ser Met Glu Met Asp
370 375 380

Asp Met Asp Leu Gly Asp Gln Asp Trp Leu Leu Gly Ser Thr Arg Lys
385 390 395 400

Pro Asp Ala Gly Ile Gly Asn Cys Arg Glu Ile Val Asp Pro Leu Thr
405 410 415

Ser Gln Ser Ala Glu Gln Phe Ser Leu Gln Pro Arg Ala Ile His Leu
420 425 430

Pro Asp Leu His Val Tyr Gln Leu Pro Tyr Val Val Pro Phe
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<213> Oryza rufipogon strain IRCG105491

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Val Val Ala Val Ala Ala Ala Glu Ala Gln Ala Thr Thr Lys Leu Gln
20 25 30

aaa gaa agg gaa aag gcc gaa aag aag aaa gag aaa aag agt gac agg 144
Lys Glu Arg Glu Lys Ala Glu Lys Lys Lys Glu Lys Lys Ser Asp Arg
35 40 45

aaa gct ctt cca cat ggt gag ata tcc aag cat tca aag cga acc cac 192

Lys	Ala	Leu	Pro	His	Gly	Glu	Ile	Ser	Lys	His	Ser	Lys	Arg	Thr	His	
50						55					60					
aag	aag	aga	aaa	cat	gaa	gac	atc	aat	aat	gct	gat	cag	aag	tcc	cgg	240
Lys	Lys	Arg	Lys	His	Glu	Asp	Ile	Asn	Asn	Ala	Asp	Gln	Lys	Ser	Arg	
65					70					75					80	
aag	gtt	tcc	tcc	atg	gaa	cct	ggt	gag	caa	ttg	gag	aag	agt	gga	ctc	288
Lys	Val	Ser	Ser	Met	Glu	Pro	Gly	Glu	Gln	Leu	Glu	Lys	Ser	Gly	Leu	
				85					90					95		
tca	gaa	gag	cat	gga	gct	cct	tgc	ttt	act	cag	aca	gtg	cat	ggc	tct	336
Ser	Glu	Glu	His	Gly	Ala	Pro	Cys	Phe	Thr	Gln	Thr	Val	His	Gly	Ser	
			100					105					110			
cca	gag	agt	tca	cag	gac	agc	agc	aag	aga	aga	aag	gtt	gtg	tta	ccc	384
Pro	Glu	Ser	Ser	Gln	Asp	Ser	Ser	Lys	Arg	Arg	Lys	Val	Val	Leu	Pro	
		115					120					125				
agt	cct	agc	caa	gct	aag	aat	ggt	aac	atc	ctt	cga	ata	aag	ata	aga	432
Ser	Pro	Ser	Gln	Ala	Lys	Asn	Gly	Asn	Ile	Leu	Arg	Ile	Lys	Ile	Arg	
	130					135					140					
aga	gat	caa	gat	tct	tca	gct	tcc	ctt	tcg	gag	aaa	tct	aat	gtt	gta	480
Arg	Asp	Gln	Asp	Ser	Ser	Ala	Ser	Leu	Ser	Glu	Lys	Ser	Asn	Val	Val	
145					150					155					160	
caa	aca	cca	gtt	cat	caa	atg	gga	tca	gtt	tca	tct	ctg	cca	agt	aag	528
Gln	Thr	Pro	Val	His	Gln	Met	Gly	Ser	Val	Ser	Ser	Leu	Pro	Ser	Lys	
				165				170						175		
aaa	aac	tca	atg	caa	cca	cac	aac	acc	gaa	atg	atg	gtg	aga	aca	gca	576
Lys	Asn	Ser	Met	Gln	Pro	His	Asn	Thr	Glu	Met	Met	Val	Arg	Thr	Ala	
			180					185					190			
tca	acc	cag	cag	caa	agc	atc	aaa	ggt	gat	ttt	caa	gca	gta	ctg	aaa	624
Ser	Thr	Gln	Gln	Gln	Ser	Ile	Lys	Gly	Asp	Phe	Gln	Ala	Val	Leu	Lys	
		195					200					205				
caa	ggt	atg	cca	acc	cca	gca	aaa	gtc	atg	cca	aga	gtc	gat	gtt	cct	672
Gln	Gly	Met	Pro	Thr	Pro	Ala	Lys	Val	Met	Pro	Arg	Val	Asp	Val	Pro	
	210					215					220					
cca	tct	atg	agg	gca	tca	aag	gaa	agg	gtt	ggc	ctt	cgt	cct	gca	gag	720
Pro	Ser	Met	Arg	Ala	Ser	Lys	Glu	Arg	Val	Gly	Leu	Arg	Pro	Ala	Glu	
225					230					235					240	
atg	ttg	gcc	aat	gtt	ggt	cct	tca	cca	tcc	aag	gca	aaa	cag	att	gtc	768
Met	Leu	Ala	Asn	Val	Gly	Pro	Ser	Pro	Ser	Lys	Ala	Lys	Gln	Ile	Val	
				245					250					255		
aat	cct	gca	gct	gct	aag	gtt	aca	caa	aga	gtt	gat	cct	cca	cct	gcc	816
Asn	Pro	Ala	Ala	Ala	Lys	Val	Thr	Gln	Arg	Val	Asp	Pro	Pro	Pro	Ala	
			260					265				270				
aag	gca	tct	cag	aga	att	gat	cct	ctg	ttg	cca	tcc	aag	gtt	cat	ata	864
Lys	Ala	Ser	Gln	Arg	Ile	Asp	Pro	Leu	Leu	Pro	Ser	Lys	Val	His	Ile	

275	280	285	
gat gct act cga tct ttt acg aag gtc tcc cag aca gag atc aag ccg Asp Ala Thr Arg Ser Phe Thr Lys Val Ser Gln Thr Glu Ile Lys Pro 290 295 300			912
gaa gta cag ccc cca att ccg aag gtg cct gtg gct atg cct acc atc Glu Val Gln Pro Pro Ile Pro Lys Val Pro Val Ala Met Pro Thr Ile 305 310 315 320			960
aat cgt cag cag att gac acc tcg cag ccc aaa gaa gag cct tgc tcc Asn Arg Gln Gln Ile Asp Thr Ser Gln Pro Lys Glu Glu Pro Cys Ser 325 330 335			1008
tct ggc agg aat gct gaa gct gct tca gta tca gta gag aag cag tcc Ser Gly Arg Asn Ala Glu Ala Ala Ser Val Ser Val Glu Lys Gln Ser 340 345 350			1056
aag tca gat cgc aaa aag agc cgc aag gct gag aag aaa gag aag aag Lys Ser Asp Arg Lys Lys Ser Arg Lys Ala Glu Lys Lys Glu Lys Lys 355 360 365			1104
ttc aaa gat tta ttt gtt acc tgg gat cct ccg tct atg gaa atg gat Phe Lys Asp Leu Phe Val Thr Trp Asp Pro Pro Ser Met Glu Met Asp 370 375 380			1152
gat atg gat ctt ggg gac cag gat tgg ctg ctt ggt agt acg agg aaa Asp Met Asp Leu Gly Asp Gln Asp Trp Leu Leu Gly Ser Thr Arg Lys 385 390 395 400			1200
cct gat gct ggc att ggc aac tgc aga gaa att gtt gat cca ctt act Pro Asp Ala Gly Ile Gly Asn Cys Arg Glu Ile Val Asp Pro Leu Thr 405 410 415			1248
tct caa tca gca gag cag ttc tca ttg cag cct agg gcg att cat tta Ser Gln Ser Ala Glu Gln Phe Ser Leu Gln Pro Arg Ala Ile His Leu 420 425 430			1296
cca gac ctt cat gtc tat cag ttg cca tat gtg gtt cca ttc tag Pro Asp Leu His Val Tyr Gln Leu Pro Tyr Val Val Pro Phe 435 440 445			1341

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 <212> PRT
 <213> Oryza rufipogon strain IRCG105491

<400> 32

Met	Ser	Arg	Cys	Phe	Pro	Tyr	Pro	Pro	Pro	Gly	Tyr	Val	Arg	Asn	Pro
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Val	Val	Ala	Val	Ala	Ala	Ala	Glu	Ala	Gln	Ala	Thr	Thr	Lys	Leu	Gln
		20					25						30		

206T20-2405200T

Lys Glu Arg Glu Lys Ala Glu Lys Lys Lys Glu Lys Lys Ser Asp Arg
35 40 45

Lys Ala Leu Pro His Gly Glu Ile Ser Lys His Ser Lys Arg Thr His
50 55 60

Lys Lys Arg Lys His Glu Asp Ile Asn Asn Ala Asp Gln Lys Ser Arg
65 70 75 80

Lys Val Ser Ser Met Glu Pro Gly Glu Gln Leu Glu Lys Ser Gly Leu
85 90 95

Ser Glu Glu His Gly Ala Pro Cys Phe Thr Gln Thr Val His Gly Ser
100 105 110

Pro Glu Ser Ser Gln Asp Ser Ser Lys Arg Arg Lys Val Val Leu Pro
115 120 125

Ser Pro Ser Gln Ala Lys Asn Gly Asn Ile Leu Arg Ile Lys Ile Arg
130 135 140

Arg Asp Gln Asp Ser Ser Ala Ser Leu Ser Glu Lys Ser Asn Val Val
145 150 155 160

Gln Thr Pro Val His Gln Met Gly Ser Val Ser Ser Leu Pro Ser Lys
165 170 175

Lys Asn Ser Met Gln Pro His Asn Thr Glu Met Met Val Arg Thr Ala
180 185 190

Ser Thr Gln Gln Gln Ser Ile Lys Gly Asp Phe Gln Ala Val Leu Lys
195 200 205

Gln Gly Met Pro Thr Pro Ala Lys Val Met Pro Arg Val Asp Val Pro
210 215 220

Pro Ser Met Arg Ala Ser Lys Glu Arg Val Gly Leu Arg Pro Ala Glu
225 230 235 240

Met Leu Ala Asn Val Gly Pro Ser Pro Ser Lys Ala Lys Gln Ile Val
245 250 255

Asn Pro Ala Ala Ala Lys Val Thr Gln Arg Val Asp Pro Pro Pro Ala
260 265 270

Lys Ala Ser Gln Arg Ile Asp Pro Leu Leu Pro Ser Lys Val His Ile
275 280 285

Asp Ala Thr Arg Ser Phe Thr Lys Val Ser Gln Thr Glu Ile Lys Pro
290 295 300

Glu Val Gln Pro Pro Ile Pro Lys Val Pro Val Ala Met Pro Thr Ile
305 310 315 320

Asn Arg Gln Gln Ile Asp Thr Ser Gln Pro Lys Glu Glu Pro Cys Ser
325 330 335

Ser Gly Arg Asn Ala Glu Ala Ala Ser Val Ser Val Glu Lys Gln Ser
340 345 350

Lys Ser Asp Arg Lys Lys Ser Arg Lys Ala Glu Lys Lys Glu Lys Lys
355 360 365

Phe Lys Asp Leu Phe Val Thr Trp Asp Pro Pro Ser Met Glu Met Asp
370 375 380

Asp Met Asp Leu Gly Asp Gln Asp Trp Leu Leu Gly Ser Thr Arg Lys
385 390 395 400

Pro Asp Ala Gly Ile Gly Asn Cys Arg Glu Ile Val Asp Pro Leu Thr
405 410 415

Ser Gln Ser Ala Glu Gln Phe Ser Leu Gln Pro Arg Ala Ile His Leu
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Pro Asp Leu His Val Tyr Gln Leu Pro Tyr Val Val Pro Phe
435 440 445

<210> 33

<211> 180

<212> DNA

<213> Zea mays mays strain BS7

<400> 33

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gatcgtttgt tcaatctgta ggttttgcgc ggatctgtgt gtttgcgcgt gcgtgatgtg 180

<210> 34

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<213> Zea mays mays strain BS7

<400> 34

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aaagcacagc cataagaaga gaaagcttga agatgtcatc aaagctgagc aggggtcccaa 180

aagagtaccc aaagaatcag ttgagcagtt ggagaagagt ggactctcag aagagcatgg 240

agctccttct tttgtacata cgatacgtga ctctcctgag agctcacagg acagcggcaa 300

gagacgaaaag gttgtcctgt ccagtcttag ccaacctaa aatggtgaga ctattctctt 360

gtttttgcta ttctgattga ttttttatta tagaagaaat caatcgcttg ttcaggattt 420

tattcatccc aacttgattt tacaggaaac attcttcgct tcaagattaa aagtagtcaa 480

gayccccaat cagctgttct ggagaaacca agggttcttg agcaaccatt ggtccaacaa 540

atgggatcag gttcatcccy gtcgggcaag caaaattcaa tccatcataa gatgaatgtg 600

agatctacct ctggtcagcg gagggctgat ggtgactccc aagcagtaca aaaatgtttg 660

attacagaat ccccggc aaa gaccatgcag agacttgtcc cccagcctgc agctaaggtc 720

acacatcctg ttgatcccca gtcagctgtt aagggtgccag ttggaagatc gggcctacct 780

ctgaagtctt cggaagtgt ggacccttcg cctgctagag ttatgagaag atttgatcct 840

ccacctgtta agatgatgtc acagagagtt caccatccag cttccatggg gtcgcagaaa 900

gttgatcctc cgtttccgaa ggtattacat aaggaaaccg gatctgttgt tcgcctacca 960

gaagctaccc ggcctactgt tcttcaaaaa cccaaggact tgcttgctat caagcagcag 1020

gatatcagga cctcttctc aaaagaagag ccctgcttct ctggtaggaa tgcagaagca 1080

gttcaagtgc aagatactaa gctctcccgg tcagacatga agaaaatccg caaagctgag 1140

aaaaaagata agaagttcag agatctgttt gttacctgga atccggtatt gatagagaat 1200

gaaggttcag atottggtga tgaagactgg ctgttcagca gtaaaaggaa ctccgatgct 1260

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aagccttctt tacaaccag ggcaacattt ttgccggacc ttaatatgta ccagctgcc 1380

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1447

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 <212> DNA
 <213> Zea mays mays strain BS7

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 Val Ala Val Ala Glu Pro Glu Ser Thr Ala Lys Leu Leu Lys Glu Lys
 20 25 30
 gaa aag gcc gaa aag aag aaa gag aaa agg agt gac agg aaa gct ccc 144
 Glu Lys Ala Glu Lys Lys Lys Glu Lys Arg Ser Asp Arg Lys Ala Pro
 35 40 45
 aag cag tgt gag acg tcc aaa cat tca aag cac agc cat aag aag aga 192
 Lys Gln Cys Glu Thr Ser Lys His Ser Lys His Ser His Lys Lys Arg
 50 55 60
 aag ctt gaa gat gtc atc aaa gct gag cag ggt ccc aaa aga gta ccc 240
 Lys Leu Glu Asp Val Ile Lys Ala Glu Gln Gly Pro Lys Arg Val Pro
 65 70 75 80
 aaa gaa tca gtt gag cag ttg gag aag agt gga ctc tca gaa gag cat 288
 Lys Glu Ser Val Glu Gln Leu Glu Lys Ser Gly Leu Ser Glu Glu His
 85 90 95
 gga gct cct tct ttt gta cat acg ata cgt gac tct cct gag agc tca 336
 Gly Ala Pro Ser Phe Val His Thr Ile Arg Asp Ser Pro Glu Ser Ser
 100 105 110
 cag gac agc ggc aag aga cga aag gtt gtc ctg tcc agt cct agc caa 384
 Gln Asp Ser Gly Lys Arg Arg Lys Val Val Leu Ser Ser Pro Ser Gln
 115 120 125
 cct aag aat gga aac att ctt cgc ttc aag att aaa agt agt caa gay 432
 Pro Lys Asn Gly Asn Ile Leu Arg Phe Lys Ile Lys Ser Ser Gln Asp
 130 135 140
 ccc caa tca gct gtt ctg gag aaa cca agg gtt ctt gag caa cca ttg 480
 Pro Gln Ser Ala Val Leu Glu Lys Pro Arg Val Leu Glu Gln Pro Leu
 145 150 155 160
 gtc caa caa atg gga tca ggt tca tcc cyg tcg ggc aag caa aat tca 528

205120" 24054001

Val	Gln	Gln	Met	Gly	Ser	Gly	Ser	Ser	Xaa	Ser	Gly	Lys	Gln	Asn	Ser		
				165					170					175			
atc	cat	cat	aag	atg	aat	gtg	aga	tct	acc	tct	ggt	cag	cgg	agg	gtc	576	
Ile	His	His	Lys	Met	Asn	Val	Arg	Ser	Thr	Ser	Gly	Gln	Arg	Arg	Val		
			180					185					190				
gat	ggt	gac	tcc	caa	gca	gta	caa	aaa	tgt	ttg	att	aca	gaa	tcc	ccg	624	
Asp	Gly	Asp	Ser	Gln	Ala	Val	Gln	Lys	Cys	Leu	Ile	Thr	Glu	Ser	Pro		
			195				200					205					
gca	aag	acc	atg	cag	aga	ctt	gtc	ccc	cag	cct	gca	gct	aag	gtc	aca	672	
Ala	Lys	Thr	Met	Gln	Arg	Leu	Val	Pro	Gln	Pro	Ala	Ala	Lys	Val	Thr		
	210					215					220						
cat	cct	gtt	gat	ccc	cag	tca	gct	gtt	aag	gtg	cca	gtt	gga	aga	tcg	720	
His	Pro	Val	Asp	Pro	Gln	Ser	Ala	Val	Lys	Val	Pro	Val	Gly	Arg	Ser		
225					230				235						240		
ggc	cta	cct	ctg	aag	tct	tcg	gga	agt	gtg	gac	cct	tcg	cct	gct	aga	768	
Gly	Leu	Pro	Leu	Lys	Ser	Ser	Gly	Ser	Val	Asp	Pro	Ser	Pro	Ala	Arg		
				245					250					255			
gtt	atg	aga	aga	ttt	gat	cct	cca	cct	gtt	aag	atg	atg	tca	cag	aga	816	
Val	Met	Arg	Arg	Phe	Asp	Pro	Pro	Pro	Val	Lys	Met	Met	Ser	Gln	Arg		
			260					265					270				
gtt	cac	cat	cca	gct	tcc	atg	gtg	tcg	cag	aaa	gtt	gat	cct	ccg	ttt	864	
Val	His	His	Pro	Ala	Ser	Met	Val	Ser	Gln	Lys	Val	Asp	Pro	Pro	Phe		
			275				280					285					
ccg	aag	gta	tta	cat	aag	gaa	acc	gga	tct	gtt	gtt	cgc	cta	cca	gaa	912	
Pro	Lys	Val	Leu	His	Lys	Glu	Thr	Gly	Ser	Val	Val	Arg	Leu	Pro	Glu		
	290					295					300						
gct	acc	cgg	cct	act	gtt	ctt	caa	aaa	ccc	aag	gac	ttg	cct	gct	atc	960	
Ala	Thr	Arg	Pro	Thr	Val	Leu	Gln	Lys	Pro	Lys	Asp	Leu	Pro	Ala	Ile		
305				310					315						320		
aag	cag	cag	gat	atc	agg	acc	tct	tcc	tca	aaa	gaa	gag	ccc	tgc	ttc	1008	
Lys	Gln	Gln	Asp	Ile	Arg	Thr	Ser	Ser	Ser	Lys	Glu	Glu	Pro	Cys	Phe		
				325				330						335			
tct	ggt	agg	aat	gca	gaa	gca	gtt	caa	gtg	caa	gat	act	aag	ctc	tcc	1056	
Ser	Gly	Arg	Asn	Ala	Glu	Ala	Val	Gln	Val	Gln	Asp	Thr	Lys	Leu	Ser		
			340					345						350			
cgg	tca	gac	atg	aag	aaa	atc	cgc	aaa	gct	gag	aaa	aaa	gat	aag	aag	1104	
Arg	Ser	Asp	Met	Lys	Lys	Ile	Arg	Lys	Ala	Glu	Lys	Lys	Asp	Lys	Lys		
			355				360					365					
ttc	aga	gat	ctg	ttt	gtt	acc	tgg	aat	ccg	gta	ttg	ata	gag	aat	gaa	1152	
Phe	Arg	Asp	Leu	Phe	Val	Thr	Trp	Asn	Pro	Val	Leu	Ile	Glu	Asn	Glu		
	370					375					380						
ggt	tca	gat	ctt	ggt	gat	gaa	gac	tgg	ctg	ttc	agc	agt	aaa	agg	aac	1200	
Gly	Ser	Asp	Leu	Gly	Asp	Glu	Asp	Trp	Leu	Phe	Ser	Ser	Lys	Arg	Asn		

10079641-24062001

385	390	395	400	
tcc gat gct atc atg gtt caa agc aga gct act gat agt tca gtg ccg				1248
Ser Asp Ala Ile Met Val Gln Ser Arg Ala Thr Asp Ser Ser Val Pro				
405	410		415	
atc cat cca atg gtg cag cag aag cct tct tta caa ccc agg gca aca				1296
Ile His Pro Met Val Gln Gln Lys Pro Ser Leu Gln Pro Arg Ala Thr				
420	425		430	
ttt ttg ccg gac ctt aat atg tac cag ctg cca tat gtc gta cca ttt				1344
Phe Leu Pro Asp Leu Asn Met Tyr Gln Leu Pro Tyr Val Val Pro Phe				
435	440		445	
taa				1347

<210> 36
 <211> 448
 <212> PRT
 <213> Zea mays mays strain BS7
 <220>
 <221> misc_feature
 <222> (170)..(170)
 <223> The 'Xaa' at location 170 stands for Pro, or Leu.

<400> 36

Met Ser Arg Cys Phe Pro Tyr Pro Pro Pro Gly Tyr Val Arg Asn Pro				
1	5	10		15
Val Ala Val Ala Glu Pro Glu Ser Thr Ala Lys Leu Leu Lys Glu Lys				
20	25		30	
Glu Lys Ala Glu Lys Lys Lys Glu Lys Arg Ser Asp Arg Lys Ala Pro				
35	40		45	
Lys Gln Cys Glu Thr Ser Lys His Ser Lys His Ser His Lys Lys Arg				
50	55		60	
Lys Leu Glu Asp Val Ile Lys Ala Glu Gln Gly Pro Lys Arg Val Pro				
65	70	75		80
Lys Glu Ser Val Glu Gln Leu Glu Lys Ser Gly Leu Ser Glu Glu His				
85	90		95	
Gly Ala Pro Ser Phe Val His Thr Ile Arg Asp Ser Pro Glu Ser Ser				
100	105		110	

Gln Asp Ser Gly Lys Arg Arg Lys Val Val Leu Ser Ser Pro Ser Gln
 115 120 125

Pro Lys Asn Gly Asn Ile Leu Arg Phe Lys Ile Lys Ser Ser Gln Asp
 130 135 140

Pro Gln Ser Ala Val Leu Glu Lys Pro Arg Val Leu Glu Gln Pro Leu
 145 150 155 160

Val Gln Gln Met Gly Ser Gly Ser Ser Xaa Ser Gly Lys Gln Asn Ser
 165 170 175

Ile His His Lys Met Asn Val Arg Ser Thr Ser Gly Gln Arg Arg Val
 180 185 190

Asp Gly Asp Ser Gln Ala Val Gln Lys Cys Leu Ile Thr Glu Ser Pro
 195 200 205

Ala Lys Thr Met Gln Arg Leu Val Pro Gln Pro Ala Ala Lys Val Thr
 210 215 220

His Pro Val Asp Pro Gln Ser Ala Val Lys Val Pro Val Gly Arg Ser
 225 230 235 240

Gly Leu Pro Leu Lys Ser Ser Gly Ser Val Asp Pro Ser Pro Ala Arg
 245 250 255

Val Met Arg Arg Phe Asp Pro Pro Pro Val Lys Met Met Ser Gln Arg
 260 265 270

Val His His Pro Ala Ser Met Val Ser Gln Lys Val Asp Pro Pro Phe
 275 280 285

Pro Lys Val Leu His Lys Glu Thr Gly Ser Val Val Arg Leu Pro Glu
 290 295 300

Ala Thr Arg Pro Thr Val Leu Gln Lys Pro Lys Asp Leu Pro Ala Ile
 305 310 315 320

Lys Gln Gln Asp Ile Arg Thr Ser Ser Ser Lys Glu Glu Pro Cys Phe
 325 330 335

Ser Gly Arg Asn Ala Glu Ala Val Gln Val Gln Asp Thr Lys Leu Ser

205T22" 2406400T

340

345

350

Arg Ser Asp Met Lys Lys Ile Arg Lys Ala Glu Lys Lys Asp Lys Lys
355 360 365

Phe Arg Asp Leu Phe Val Thr Trp Asn Pro Val Leu Ile Glu Asn Glu
370 375 380

Gly Ser Asp Leu Gly Asp Glu Asp Trp Leu Phe Ser Ser Lys Arg Asn
385 390 395 400

Ser Asp Ala Ile Met Val Gln Ser Arg Ala Thr Asp Ser Ser Val Pro
405 410 415

Ile His Pro Met Val Gln Gln Lys Pro Ser Leu Gln Pro Arg Ala Thr
420 425 430

Phe Leu Pro Asp Leu Asn Met Tyr Gln Leu Pro Tyr Val Val Pro Phe
435 440 445

<210> 37

<211> 2646

<212> DNA

<213> Zea mays mays strain HuoBai

<400> 37

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tacgtgcgga acccagtggc cgtggccgag ccggagtcga ccgctaaggt ttgttgaacc	120
ttcggattta cacacgcacg tgccagatcg tttgttcaat ctgtaggttt tgcgcggatc	180
tgtggtttgc gcgtgogtga tgtgggtatt gcccgtcct tgaaagctaa ccgagctgag	240
gaagtgtatg gatcttgtgt agctgcacga ggtcctccaa atcgattgta aaatttaagt	300
tgtatggccg gtaggccaag attgggttat tccggttttc gaaaactggg agcatgggta	360
tcggggacat tgaaagaatg gtagaacatc aaattcgatt caaaactgtg ctagatttgc	420
atatttagtc gccctaaaat tacgtggacg tgggtgatcc gaattggttg ttgtatgatg	480
gttgggaagtg actggccaaa tttttttgtt tctcaaagtt ttctttgaaa aactgtttgt	540
cgagcgtcaa ttcgtattta cctgaattta ctaattctta atacagtatg tcgttatttt	600
gggctaagct tgtgtaagaa gggtcgtttg acattttgta ctgtattgat gctgttttgt	660
gtttctttgt tcggagcagc attcaatgct ctttttggtg tttgagagaa tctgatattt	720

gccatcgtag cgaaagtccg aaaccaacta ttcaaattgg gatttcattt cttttttttt	780
ctactgtttt tagagttctc tttttcgctg ctgtgctcct gtgggtcagt acgtgcattt	840
ctcttttttt cttttttttt ctgatgttac tcttctgttg accaaaggag ttcagaatta	900
ttttggccct gtatatcaat agcaaccaac accatttatt gagcccattt ttagttttct	960
tgttctgtag agtatgcatt gttgcaggtc ttaactgttg tcagggaggt aacgtgttca	1020
acatgattgt aaacgaatac aattctgttg ctaactgtgt aatgatgaga aggataattg	1080
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gttcgtgtaa atatcattat acataaaaaat gctgcattgc attcccgtcg tccgttctaa	1200
atcagaactg acgattgctc tgggtggctga agctcctgaa agaaaaggaa aaggccgaaa	1260
agaagaaaga gaaaaggagt gacaggaaag ctcccaagca gtgtgagacg tccaaacatt	1320
caaagcacag ccataagaag agaaagcttg aagatgtcat caaagctgag cagggtccca	1380
aaagagtacc caaagaatca gttgagcagt tggagaagag tggactctca gaagagcatg	1440
gagctccttc ttttgtacat acgatacgtg actctcctga gagctcacag gacagcggca	1500
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ttattcatcc caacttgatt ttacaggaaa cattcttcgc ttcaagatta aaagtagtca	1680
agatcccca tcagctgttc tggagaaacc aagggttctt gagcaaccat tggccaaca	1740
aatgggatca ggttcatccc tgtcgggcaa gcaaaattca atccatcata agatgaatgt	1800
gagatctacc tctggtcagc ggaggggtcaa tgggtgactcc caagcagtag aaaaatgttt	1860
gattacagaa tccccggcaa agaccatgca gagacttgct cccagcctg cagctaaggt	1920
cacacatcct gttgatcccc agtcagctgt taagggtgcca gttggaagat cgggcctacc	1980
tctgaagtct tcgggaagtg tggacccttc gcctgctaga gttatgagaa gatttgatcc	2040
tccacctgtt aagatgatgt cacagagagt tcaccatcca gttccatgg tgcgcagaa	2100
agttgatcct ccgtttccga aggtattaca taaggaaacc ggatctgttg ttcgcctacc	2160
agaagctacc cggcctactg ttcttcaaaa acccaaggac ttgcctgcta tcaagcagca	2220
ggatatcagg acctcttctt caaaagaaga gccctgcttc tctggtagga atgcagaagc	2280
agttcaagtg caagatacta agctctcccg gtcagacatg aagaaaatcc gcaaagctga	2340
gaaaaaagat aagaagttca gagatctgtt tgttacctgg aatccggtat tgatagagaa	2400
tgaaggttca gatcttggtg atgaagactg gctgttcagc agtaaaagga actccgatgc	2460

tatcatgggtt caaagcagag ctactgatag ttccagtgccg atccatccaa tgggtgcagca 2520
gaagccttctt ttacaaccca gggcaacatt tttgccggac cttaatatgt accagctgcc 2580
atatgtcgta ccatttttaa catctggcga ggtagatgag aattagatga gatgttggga 2640
gagagc 2646

<210> 38
<211> 1347
<212> DNA
<213> Zea mays mays strain HuoBai

<220>
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<222> (1)..(1347)
<223>

<400> 38
atg tcg agg tgc ttc ccc tac ccg cca ccg ggg tac gtg cgg aac cca 48
Met Ser Arg Cys Phe Pro Tyr Pro Pro Pro Gly Tyr Val Arg Asn Pro
1 5 10 15
gtg gcc gtg gcc gag ccg gag tcg acc gct aag ctc ctg aaa gaa aag 96
Val Ala Val Ala Glu Pro Glu Ser Thr Ala Lys Leu Leu Lys Glu Lys
20 25 30
gaa aag gcc gaa aag aag aaa gag aaa agg agt gac agg aaa gct ccc 144
Glu Lys Ala Glu Lys Lys Lys Glu Lys Arg Ser Asp Arg Lys Ala Pro
35 40 45
aag cag tgt gag acg tcc aaa cat tca aag cac agc cat aag aag aga 192
Lys Gln Cys Glu Thr Ser Lys His Ser Lys His Ser His Lys Lys Arg
50 55 60
aag ctt gaa gat gtc atc aaa gct gag cag ggt ccc aaa aga gta ccc 240
Lys Leu Glu Asp Val Ile Lys Ala Glu Gln Gly Pro Lys Arg Val Pro
65 70 75 80
aaa gaa tca gtt gag cag ttg gag aag agt gga ctc tca gaa gag cat 288
Lys Glu Ser Val Glu Gln Leu Glu Lys Ser Gly Leu Ser Glu Glu His
85 90 95
gga gct cct tct ttt gta cat acg ata cgt gac tct cct gag agc tca 336
Gly Ala Pro Ser Phe Val His Thr Ile Arg Asp Ser Pro Glu Ser Ser
100 105 110
cag gac agc ggc aag aga cga aag gtt gtc ctg tcc agt cct agc caa 384
Gln Asp Ser Gly Lys Arg Arg Lys Val Val Leu Ser Ser Pro Ser Gln
115 120 125
cct aag aat gga aac att ctt cgc ttc aag att aaa agt agt caa gat 432
Pro Lys Asn Gly Asn Ile Leu Arg Phe Lys Ile Lys Ser Ser Gln Asp
130 135 140

ccc caa tca gct gtt ctg gag aaa cca agg gtt ctt gag caa cca ttg Pro Gln Ser Ala Val Leu Glu Lys Pro Arg Val Leu Glu Gln Pro Leu 145 150 155 160	480
gtc caa caa atg gga tca ggt tca tcc ctg tcg ggc aag caa aat tca Val Gln Gln Met Gly Ser Gly Ser Ser Leu Ser Gly Lys Gln Asn Ser 165 170 175	528
atc cat cat aag atg aat gtg aga tct acc tct ggt cag cgg agg gtc Ile His His Lys Met Asn Val Arg Ser Thr Ser Gly Gln Arg Arg Val 180 185 190	576
aat ggt gac tcc caa gca gta caa aaa tgt ttg att aca gaa tcc ccg Asn Gly Asp Ser Gln Ala Val Gln Lys Cys Leu Ile Thr Glu Ser Pro 195 200 205	624
gca aag acc atg cag aga ctt gtc ccc cag cct gca gct aag gtc aca Ala Lys Thr Met Gln Arg Leu Val Pro Gln Pro Ala Ala Lys Val Thr 210 215 220	672
cat cct gtt gat ccc cag tca gct gtt aag gtg cca gtt gga aga tcg His Pro Val Asp Pro Gln Ser Ala Val Lys Val Pro Val Gly Arg Ser 225 230 235 240	720
ggc cta cct ctg aag tct tcg gga agt gtg gac cct tcg cct gct aga Gly Leu Pro Leu Lys Ser Ser Gly Ser Val Asp Pro Ser Pro Ala Arg 245 250 255	768
gtt atg aga aga ttt gat cct cca cct gtt aag atg atg tca cag aga Val Met Arg Arg Phe Asp Pro Pro Pro Val Lys Met Met Ser Gln Arg 260 265 270	816
gtt cac cat cca gct tcc atg gtg tcg cag aaa gtt gat cct ccg ttt Val His His Pro Ala Ser Met Val Ser Gln Lys Val Asp Pro Pro Phe 275 280 285	864
ccg aag gta tta cat aag gaa acc gga tct gtt gtt cgc cta cca gaa Pro Lys Val Leu His Lys Glu Thr Gly Ser Val Val Arg Leu Pro Glu 290 295 300	912
gct acc cgg cct act gtt ctt caa aaa ccc aag gac ttg cct gct atc Ala Thr Arg Pro Thr Val Leu Gln Lys Pro Lys Asp Leu Pro Ala Ile 305 310 315 320	960
aag cag cag gat atc agg acc tct tcc tca aaa gaa gag ccc tgc ttc Lys Gln Gln Asp Ile Arg Thr Ser Ser Ser Lys Glu Glu Pro Cys Phe 325 330 335	1008
tct ggt agg aat gca gaa gca gtt caa gtg caa gat act aag ctc tcc Ser Gly Arg Asn Ala Glu Ala Val Gln Val Gln Asp Thr Lys Leu Ser 340 345 350	1056
cgg tca gac atg aag aaa atc cgc aaa gct gag aaa aaa gat aag aag Arg Ser Asp Met Lys Lys Ile Arg Lys Ala Glu Lys Lys Asp Lys Lys 355 360 365	1104

206100 2406200T

ttc aga gat ctg ttt gtt acc tgg aat ccg gta ttg ata gag aat gaa 1152
Phe Arg Asp Leu Phe Val Thr Trp Asn Pro Val Leu Ile Glu Asn Glu
370 375 380

ggg tca gat ctt ggt gat gaa gac tgg ctg ttc agc agt aaa agg aac 1200
Gly Ser Asp Leu Gly Asp Glu Asp Trp Leu Phe Ser Ser Lys Arg Asn
385 390 395 400

tcc gat gct atc atg gtt caa agc aga gct act gat agt tca gtg ccg 1248
Ser Asp Ala Ile Met Val Gln Ser Arg Ala Thr Asp Ser Ser Val Pro
405 410 415

atc cat cca atg gtg cag cag aag cct tct tta caa ccc agg gca aca 1296
Ile His Pro Met Val Gln Gln Lys Pro Ser Leu Gln Pro Arg Ala Thr
420 425 430

ttt ttg ccg gac ctt aat atg tac cag ctg cca tat gtc gta cca ttt 1344
Phe Leu Pro Asp Leu Asn Met Tyr Gln Leu Pro Tyr Val Val Pro Phe
435 440 445

taa 1347

<210> 39

<211> 448

<212> PRT

<213> Zea mays mays strain HuoBai

<400> 39

Met Ser Arg Cys Phe Pro Tyr Pro Pro Pro Gly Tyr Val Arg Asn Pro
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Val Ala Val Ala Glu Pro Glu Ser Thr Ala Lys Leu Leu Lys Glu Lys
20 25 30

Glu Lys Ala Glu Lys Lys Lys Glu Lys Arg Ser Asp Arg Lys Ala Pro
35 40 45

Lys Gln Cys Glu Thr Ser Lys His Ser Lys His Ser His Lys Lys Arg
50 55 60

Lys Leu Glu Asp Val Ile Lys Ala Glu Gln Gly Pro Lys Arg Val Pro
65 70 75 80

Lys Glu Ser Val Glu Gln Leu Glu Lys Ser Gly Leu Ser Glu Glu His
85 90 95

Gly Ala Pro Ser Phe Val His Thr Ile Arg Asp Ser Pro Glu Ser Ser
100 105 110

Gln Asp Ser Gly Lys Arg Arg Lys Val Val Leu Ser Ser Pro Ser Gln
 115 120 125

Pro Lys Asn Gly Asn Ile Leu Arg Phe Lys Ile Lys Ser Ser Gln Asp
 130 135 140

Pro Gln Ser Ala Val Leu Glu Lys Pro Arg Val Leu Glu Gln Pro Leu
 145 150 155 160

Val Gln Gln Met Gly Ser Gly Ser Ser Leu Ser Gly Lys Gln Asn Ser
 165 170 175

Ile His His Lys Met Asn Val Arg Ser Thr Ser Gly Gln Arg Arg Val
 180 185 190

Asn Gly Asp Ser Gln Ala Val Gln Lys Cys Leu Ile Thr Glu Ser Pro
 195 200 205

Ala Lys Thr Met Gln Arg Leu Val Pro Gln Pro Ala Ala Lys Val Thr
 210 215 220

His Pro Val Asp Pro Gln Ser Ala Val Lys Val Pro Val Gly Arg Ser
 225 230 235 240

Gly Leu Pro Leu Lys Ser Ser Gly Ser Val Asp Pro Ser Pro Ala Arg
 245 250 255

Val Met Arg Arg Phe Asp Pro Pro Pro Val Lys Met Met Ser Gln Arg
 260 265 270

Val His His Pro Ala Ser Met Val Ser Gln Lys Val Asp Pro Pro Phe
 275 280 285

Pro Lys Val Leu His Lys Glu Thr Gly Ser Val Val Arg Leu Pro Glu
 290 295 300

Ala Thr Arg Pro Thr Val Leu Gln Lys Pro Lys Asp Leu Pro Ala Ile
 305 310 315 320

Lys Gln Gln Asp Ile Arg Thr Ser Ser Ser Lys Glu Glu Pro Cys Phe
 325 330 335

Ser Gly Arg Asn Ala Glu Ala Val Gln Val Gln Asp Thr Lys Leu Ser
 340 345 350

Arg Ser Asp Met Lys Lys Ile Arg Lys Ala Glu Lys Lys Asp Lys Lys
 355 360 365

Phe Arg Asp Leu Phe Val Thr Trp Asn Pro Val Leu Ile Glu Asn Glu
 370 375 380

Gly Ser Asp Leu Gly Asp Glu Asp Trp Leu Phe Ser Ser Lys Arg Asn
 385 390 395 400

Ser Asp Ala Ile Met Val Gln Ser Arg Ala Thr Asp Ser Ser Val Pro
 405 410 415

Ile His Pro Met Val Gln Gln Lys Pro Ser Leu Gln Pro Arg Ala Thr
 420 425 430

Phe Leu Pro Asp Leu Asn Met Tyr Gln Leu Pro Tyr Val Val Pro Phe
 435 440 445

<210> 40
 <211> 262
 <212> DNA
 <213> Zea mays mays strain Makki
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 gagccggagt cgaccgctaa ggtttgttga accttcggat ttacacacgc acgtgccaga 180
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 attgcccggtg ccttgaaagc ta 262

<210> 41
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 <212> DNA
 <213> Zea mays mays strain Makki
 <400> 41
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 atccgaattg gttgttgtat gatggttga agtgactggc caaatttttt tgtttctcaa 180

agttttcttt gacaaactgt ttgtcgagcg tcaattcgta tttacctgaa tttactaatt	240
cttaatacag tatgtcgta ttttgggcta agcttgtgta agaagggtcg tttgacattt	300
tgtactgtat tgatgctgtt ttgtgtttct ttgttcggag cagcattcaa tgctcctttt	360
gttgtttgag agaatctgat atttgccatc gtaccgaaag tccgaaacca actattcaaa	420
ttgggatttc atttcttttt ttttctactg tttttagagt tctctttttc gctgctgtgc	480
tcttgtgggt cagtacgtgc atttctcttt ttttcttttt ttttctgatg ttactcttct	540
gttgacccaa ggagttcaga attatttttg acctgtatat caatagcaac caacaccatt	600
tattgagccc atttttagtt ttcttgttct gtagagtatg cattgttgca ggtcttaact	660
gttgtcaggg aagtaacgtg ttcaacatga ttgtaaacga atacaattct gttgctaact	720
gtgtaatgat gagaaggata attgaataat ctttgtgaag tattactgtc tgaactgtac	780
gcaaattgcta cattcattct ttgtgttcgt gtaaatatca ttatacataa aaatgctgca	840
ttgcattccc gtcgtccgtt ctaaatacaga actgacgatt gctctgggtg ctgaagctcc	900
tgaaagaaaa ggaaaaggcc gaaaagaaga aagagaaaag gagtgacagg aaagctccca	960
agcagtgtga gacgtccaaa cattcaaagc acagccataa gaagagaaaag cttgaagatg	1020
tcatcaaagc tgagcagggg cccaaaagag tacccaaaga atcagttgag cagttggaga	1080
agagtggact ctcagaagag catggagctc cttcttttgt acatacgata cgtgactctc	1140
ctgagagctc acaggacagc ggcaagagac gaaaggttgt cctgtccagt cctagccaac	1200
ctaagaatgg tgagactatt ctcttgtttt tgctattctg attgattttt tattatagaa	1260
gaaatcaatc gcttgttcag gattttattc atcccaactt gattttacag gaaacattct	1320
tcgcttcaag attaaaagta gtcaagatcc ccaatcagct gttctggaga aaccaagggt	1380
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ctcccaagca gtacaaaaat gtttgattac agaatccccg gcaaagacca tgcagagact	1560
tgtccccccag cctgcagcta aggtcacaca tcctgttgat cccagtcag ctgttaaggt	1620
gccagttgga agatcgggccc tacctctgaa gtcttcrgga agtgtggacc ctctgcctgc	1680
tagagttatg agaagatttg atcctccacc tgttaagatg atgtcacaga gagttcacca	1740
tccagcttcc atgggtgtcg agaaagttga tcctccgttt ccgaaggtat tacataagga	1800
aaccggatct gttgttcgcc taccagaagc taccggcct actgttcttc aaaaacccaa	1860
ggacttgcct gctatcaagc agcaggatat caggacctct tcctcaaaag aagagccctg	1920

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cttctctggt aggaatgcag aagcagttca agtgcaagat actaagctct cccggtcaga 1980
catgaagaaa atccgcaaag ctgagaaaaa agataagaag ttcagagatc tgtttggttac 2040
ctggaatccg gtattgatag agaatgaagg ttcagatctt ggtgatgaag actggctggt 2100
cagcagtaaa aggaactccg atgctatcat ggttcaaagc agagctactg atagttcagt 2160
gccgatccat ccaatgggtgc agcagaagcc ttctttacaa cccagggcaa catttttgcc 2220
ggaccttaat atgtaccagc tgccatatgt cgtaccattt taaacatctg gcgaggtaga 2280
tgagaattag atgagatggt gggagagagc t 2311

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<210> 42
<211> 1347
<212> DNA
<213> Zea mays mays strain Makki

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<220>
<221> CDS
<222> (1)..(1347)
<223>

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<400> 42
atg tcg agg tgc ttc ccc tac ccg cca ccg ggg tac gtg cgg aac cca 48
Met Ser Arg Cys Phe Pro Tyr Pro Pro Gly Tyr Val Arg Asn Pro
1 5 10 15

gtg gcc gtg gcc gag ccg gag tcg acc gct aag ctc ctg aaa gaa aag 96
Val Ala Val Ala Glu Pro Glu Ser Thr Ala Lys Leu Leu Lys Glu Lys
20 25 30

gaa aag gcc gaa aag aag aaa gag aaa agg agt gac agg aaa gct ccc 144
Glu Lys Ala Glu Lys Lys Lys Glu Lys Arg Ser Asp Arg Lys Ala Pro
35 40 45

aag cag tgt gag acg tcc aaa cat tca aag cac agc cat aag aag aga 192
Lys Gln Cys Glu Thr Ser Lys His Ser Lys His Ser His Lys Lys Arg
50 55 60

aag ctt gaa gat gtc atc aaa gct gag cag ggt ccc aaa aga gta ccc 240
Lys Leu Glu Asp Val Ile Lys Ala Glu Gln Gly Pro Lys Arg Val Pro
65 70 75 80

aaa gaa tca gtt gag cag ttg gag aag agt gga ctc tca gaa gag cat 288
Lys Glu Ser Val Glu Gln Leu Glu Lys Ser Gly Leu Ser Glu Glu His
85 90 95

gga gct cct tct ttt gta cat acg ata cgt gac tct cct gag agc tca 336
Gly Ala Pro Ser Phe Val His Thr Ile Arg Asp Ser Pro Glu Ser Ser
100 105 110

cag gac agc ggc aag aga cga aag gtt gtc ctg tcc agt cct agc caa 384

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Gln Asp Ser Gly Lys Arg Arg Lys Val Val Leu Ser Ser Pro Ser Gln	
115 120 125	
cct aag aat gga aac att ctt cgc ttc aag att aaa agt agt caa gat	432
Pro Lys Asn Gly Asn Ile Leu Arg Phe Lys Ile Lys Ser Ser Gln Asp	
130 135 140	
ccc caa tca gct gtt ctg gag aaa cca agg gtt ctt gag caa cca ttg	480
Pro Gln Ser Ala Val Leu Glu Lys Pro Arg Val Leu Glu Gln Pro Leu	
145 150 155 160	
gtc caa caa atg gga tca ggt tca tcc ctg tct ggc aag caa aat tca	528
Val Gln Gln Met Gly Ser Gly Ser Ser Leu Ser Gly Lys Gln Asn Ser	
165 170 175	
atc cat cat aag atg aat gtg aga tct acc tct ggt cag cgg agg gtc	576
Ile His His Lys Met Asn Val Arg Ser Thr Ser Gly Gln Arg Arg Val	
180 185 190	
aat ggt gac tcc caa gca gta caa aaa tgt ttg att aca gaa tcc ccg	624
Asn Gly Asp Ser Gln Ala Val Gln Lys Cys Leu Ile Thr Glu Ser Pro	
195 200 205	
gca aag acc atg cag aga ctt gtc ccc cag cct gca gct aag gtc aca	672
Ala Lys Thr Met Gln Arg Leu Val Pro Gln Pro Ala Ala Lys Val Thr	
210 215 220	
cat cct gtt gat ccc cag tca gct gtt aag gtg cca gtt gga aga tcg	720
His Pro Val Asp Pro Gln Ser Ala Val Lys Val Pro Val Gly Arg Ser	
225 230 235 240	
ggc cta cct ctg aag tct tcr gga agt gtg gac cct tcg cct gct aga	768
Gly Leu Pro Leu Lys Ser Xaa Gly Ser Val Asp Pro Ser Pro Ala Arg	
245 250 255	
gtt atg aga aga ttt gat cct cca cct gtt aag atg atg tca cag aga	816
Val Met Arg Arg Phe Asp Pro Pro Pro Val Lys Met Met Ser Gln Arg	
260 265 270	
gtt cac cat cca gct tcc atg gtg tcg cag aaa gtt gat cct ccg ttt	864
Val His His Pro Ala Ser Met Val Ser Gln Lys Val Asp Pro Pro Phe	
275 280 285	
ccg aag gta tta cat aag gaa acc gga tct gtt gtt cgc cta cca gaa	912
Pro Lys Val Leu His Lys Glu Thr Gly Ser Val Val Arg Leu Pro Glu	
290 295 300	
gct acc cgg cct act gtt ctt caa aaa ccc aag gac ttg cct gct atc	960
Ala Thr Arg Pro Thr Val Leu Gln Lys Pro Lys Asp Leu Pro Ala Ile	
305 310 315 320	
aag cag cag gat atc agg acc tct tcc tca aaa gaa gag ccc tgc ttc	1008
Lys Gln Gln Asp Ile Arg Thr Ser Ser Ser Lys Glu Glu Pro Cys Phe	
325 330 335	
tct ggt agg aat gca gaa gca gtt caa gtg caa gat act aag ctc tcc	1056
Ser Gly Arg Asn Ala Glu Ala Val Gln Val Gln Asp Thr Lys Leu Ser	

340	345	350	
cgg tca gac atg aag aaa atc cgc aaa gct gag aaa aaa gat aag aag			1104
Arg Ser Asp Met Lys Lys Ile Arg Lys Ala Glu Lys Lys Asp Lys Lys			
355	360	365	
ttc aga gat ctg ttt gtt acc tgg aat ccg gta ttg ata gag aat gaa			1152
Phe Arg Asp Leu Phe Val Thr Trp Asn Pro Val Leu Ile Glu Asn Glu			
370	375	380	
ggg tca gat ctt ggt gat gaa gac tgg ctg ttc agc agt aaa agg aac			1200
Gly Ser Asp Leu Gly Asp Glu Asp Trp Leu Phe Ser Ser Lys Arg Asn			
385	390	400	
tcc gat gct atc atg gtt caa agc aga gct act gat agt tca gtg ccg			1248
Ser Asp Ala Ile Met Val Gln Ser Arg Ala Thr Asp Ser Ser Val Pro			
405	410	415	
atc cat cca atg gtg cag cag aag cct tct tta caa ccc agg gca aca			1296
Ile His Pro Met Val Gln Gln Lys Pro Ser Leu Gln Pro Arg Ala Thr			
420	425	430	
ttt ttg ccg gac ctt aat atg tac cag ctg cca tat gtc gta cca ttt			1344
Phe Leu Pro Asp Leu Asn Met Tyr Gln Leu Pro Tyr Val Val Pro Phe			
435	440	445	
taa			1347

<210> 43
 <211> 448
 <212> PRT
 <213> Zea mays mays strain Makki
 <220>
 <221> misc_feature
 <222> (247)..(247)
 <223> The 'Xaa' at location 247 stands for Ser.
 <400> 43

Met Ser Arg Cys Phe Pro Tyr Pro Pro Pro Gly Tyr Val Arg Asn Pro	
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Val Ala Val Ala Glu Pro Glu Ser Thr Ala Lys Leu Leu Lys Glu Lys	
20 25 30	
Glu Lys Ala Glu Lys Lys Lys Glu Lys Arg Ser Asp Arg Lys Ala Pro	
35 40 45	
Lys Gln Cys Glu Thr Ser Lys His Ser Lys His Ser His Lys Lys Arg	
50 55 60	

1004042001

Lys Leu Glu Asp Val Ile Lys Ala Glu Gln Gly Pro Lys Arg Val Pro
65 70 75 80

Lys Glu Ser Val Glu Gln Leu Glu Lys Ser Gly Leu Ser Glu Glu His
85 90 95

Gly Ala Pro Ser Phe Val His Thr Ile Arg Asp Ser Pro Glu Ser Ser
100 105 110

Gln Asp Ser Gly Lys Arg Arg Lys Val Val Leu Ser Ser Pro Ser Gln
115 120 125

Pro Lys Asn Gly Asn Ile Leu Arg Phe Lys Ile Lys Ser Ser Gln Asp
130 135 140

Pro Gln Ser Ala Val Leu Glu Lys Pro Arg Val Leu Glu Gln Pro Leu
145 150 155 160

Val Gln Gln Met Gly Ser Gly Ser Ser Leu Ser Gly Lys Gln Asn Ser
165 170 175

Ile His His Lys Met Asn Val Arg Ser Thr Ser Gly Gln Arg Arg Val
180 185 190

Asn Gly Asp Ser Gln Ala Val Gln Lys Cys Leu Ile Thr Glu Ser Pro
195 200 205

Ala Lys Thr Met Gln Arg Leu Val Pro Gln Pro Ala Ala Lys Val Thr
210 215 220

His Pro Val Asp Pro Gln Ser Ala Val Lys Val Pro Val Gly Arg Ser
225 230 235 240

Gly Leu Pro Leu Lys Ser Xaa Gly Ser Val Asp Pro Ser Pro Ala Arg
245 250 255

Val Met Arg Arg Phe Asp Pro Pro Pro Val Lys Met Met Ser Gln Arg
260 265 270

Val His His Pro Ala Ser Met Val Ser Gln Lys Val Asp Pro Pro Phe
275 280 285

Pro Lys Val Leu His Lys Glu Thr Gly Ser Val Val Arg Leu Pro Glu

290

295

300

Ala Thr Arg Pro Thr Val Leu Gln Lys Pro Lys Asp Leu Pro Ala Ile
305 310 315 320

Lys Gln Gln Asp Ile Arg Thr Ser Ser Ser Lys Glu Glu Pro Cys Phe
325 330 335

Ser Gly Arg Asn Ala Glu Ala Val Gln Val Gln Asp Thr Lys Leu Ser
340 345 350

Arg Ser Asp Met Lys Lys Ile Arg Lys Ala Glu Lys Lys Asp Lys Lys
355 360 365

Phe Arg Asp Leu Phe Val Thr Trp Asn Pro Val Leu Ile Glu Asn Glu
370 375 380

Gly Ser Asp Leu Gly Asp Glu Asp Trp Leu Phe Ser Ser Lys Arg Asn
385 390 395 400

Ser Asp Ala Ile Met Val Gln Ser Arg Ala Thr Asp Ser Ser Val Pro
405 410 415

Ile His Pro Met Val Gln Gln Lys Pro Ser Leu Gln Pro Arg Ala Thr
420 425 430

Phe Leu Pro Asp Leu Asn Met Tyr Gln Leu Pro Tyr Val Val Pro Phe
435 440 445

<210> 44

<211> 125

<212> DNA

<213> Zea mays mays strain Min13

<400> 44

ctttgtgac tctcggcggg gtagagcgcg gtcgaccgtc ggccatgtcg aggtgcttcc 60

cctaccgcgc accgggggtac gtgcggaacc cagtggccgt ggccgagccg gattcgaccg 120

ctaag 125

<210> 45

<211> 198

<212> DNA

<213> Zea mays mays strain Min13

<400> 45

cttaatacag tatgtcggtta ttttgggcta agcttgtgta agaaggggtcg tttgacattt 60
 tgtactgtat tgatgctgtt ttgtgtttct ttgttcggag cagcattcaa tgctcctttt 120
 gttgtttgag agaatctgat atttgccatc gtaccgaaag tccgaaacca actattcaaa 180
 ttgggatttc atttcttt 198

<210> 46

<211> 1787

<212> DNA

<213> Zea mays mays strain Min13

<400> 46

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 atagcaacca acaccattta ttgagcccat ttttagtttt cttgttctgt agagtatgca 120
 ttgttgcagg tcttaactgt tgtcagggaa gtaacgtgtt caacatgatt gtaaacgaat 180
 acaattctgt tgctaactgt gtaatgatga gaaggataat tgaataatct ttgtgaagta 240
 ttactgtctg aactgtacgc aaatgctaca ttcattcttt gtgttcgtgt aaatatcatt 300
 atacataaaa atgctgcatt gcattcccgt cgtccgttct aaatcagaac tgacgattgc 360
 tctggtggct gaagctcctg aaagaaaagg aaaaggccga aaagaagaaa gagaaaagga 420
 gtgacaggaa agtcccaaag cagtgtgaga cgtccaaaca ttcaaagcac agccataaga 480
 agagaaagct tgaagatgtc atcaaagctg agcaggggtcc caaaagagta cccaaagaat 540
 cagttgagca gttggagaag agtggactct cagaagagca tggagctcct tcttttgtac 600
 atacgatacg tgactctcct gagagctcac aggacagcgg caagagacga aaggttgtcc 660
 tgtccagtcc tagccaacct aagaatggtg agactattct cttgtttttg ctattctgat 720
 tgatttttta ttatagaaga aatcaatcgc ttgttcagga ttttattcat cccaacttga 780
 ttttacagga aacattcttc gcttcaagat taaaagtagt caagatcccc aatcagctgt 840
 tctggagaaa ccaagggttc ttgagcaacc attggtccaa caaatgggat caggttcac 900
 cctgtcgggc aagcaaaatt caatccatca taagatgaat gtgagatcta cctctggtca 960
 gcggagggtc aatggtgact cccaagcagt acaaaaatgt ttgattacag aatccccggc 1020
 aaagaccatg cagagacttg tccccagcc tgcagctaag gtcacacatc ctgttgatcc 1080
 ccagtcagct gttaagggtc cagttggaag atcgggccta cctctgaagt cttcgggaag 1140
 tgtggaccct tcgcctgcta gagttatgag aagatttgat cctccacctg ttaagatgat 1200
 gtcacagaga gttcaccatc cagcttccat ggtgtcgcag aaagttgatc ctccgtttcc 1260

gaaggtatta cataaggaaa ccggatctgt tgttcgccta ccagaagcta cccggcctac 1320
 tgtttcttcaa aaacccaagg acttgctgc tatcaagcag caggatatca ggacctcttc 1380
 ctcaaaagaa gagccctgct tctctggtag gaatgcagaa gcagttcaag tgcaggatac 1440
 taagctctcc cggtcagaya tgaagaaaat ccgcaaagct gagaaaaaag ataagaagtt 1500
 cagagatctg tttgttacct ggaatccggt attgatagag aatgaaggtt cagatcttgg 1560
 tgatgaagac tggctgttca gcagtaaaag gaactccgat gctatcatgg ttcaaagcag 1620
 agctactgat agttcagtgc cgatccatcc aatggtgcag cagaagcctt ctttacaacc 1680
 cagggcaaca tttttgccgg accttaatat gtaccagctg ccataatgtcg taccatttta 1740
 aacatctggc gaggtagatg agaattagat gagatgttgg gagagag 1787

<210> 47
 <211> 1347
 <212> DNA
 <213> Zea mays mays strain Min13

<220>
 <221> CDS
 <222> (1)..(1347)
 <223>

<400> 47
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 Met Ser Arg Cys Phe Pro Tyr Pro Pro Pro Gly Tyr Val Arg Asn Pro
 1 5 10 15
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 Val Ala Val Ala Glu Pro Glu Ser Thr Ala Lys Leu Leu Lys Glu Lys
 20 25 30
 gaa aag gcc gaa aag aag aaa gag aaa agg agt gac agg aaa gct ccc 144
 Glu Lys Ala Glu Lys Lys Lys Glu Lys Arg Ser Asp Arg Lys Ala Pro
 35 40 45
 aag cag tgt gag acg tcc aaa cat tca aag cac agc cat aag aag aga 192
 Lys Gln Cys Glu Thr Ser Lys His Ser Lys His Ser His Lys Lys Arg
 50 55 60
 aag ctt gaa gat gtc atc aaa gct gag cag ggt ccc aaa aga gta ccc 240
 Lys Leu Glu Asp Val Ile Lys Ala Glu Gln Gly Pro Lys Arg Val Pro
 65 70 75 80
 aaa gaa tca gtt gag cag ttg gag aag agt gga ctc tca gaa gag cat 288
 Lys Glu Ser Val Glu Gln Leu Glu Lys Ser Gly Leu Ser Glu Glu His
 85 90 95
 gga gct cct tct ttt gta cat acg ata cgt gac tct cct gag agc tca 336

Gly Ala Pro Ser Phe Val His Thr Ile Arg Asp Ser Pro Glu Ser Ser	
100 105 110	
cag gac agc ggc aag aga cga aag gtt gtc ctg tcc agt cct agc caa	384
Gln Asp Ser Gly Lys Arg Arg Lys Val Val Leu Ser Ser Pro Ser Gln	
115 120 125	
cct aag aat gga aac att ctt cgc ttc aag att aaa agt agt caa gat	432
Pro Lys Asn Gly Asn Ile Leu Arg Phe Lys Ile Lys Ser Ser Gln Asp	
130 135 140	
ccc caa tca gct gtt ctg gag aaa cca agg gtt ctt gag caa cca ttg	480
Pro Gln Ser Ala Val Leu Glu Lys Pro Arg Val Leu Glu Gln Pro Leu	
145 150 155 160	
gtc caa caa atg gga tca ggt tca tcc ctg tcg ggc aag caa aat tca	528
Val Gln Gln Met Gly Ser Gly Ser Ser Leu Ser Gly Lys Gln Asn Ser	
165 170 175	
atc cat cat aag atg aat gtg aga tct acc tct ggt cag cgg agg gtc	576
Ile His His Lys Met Asn Val Arg Ser Thr Ser Gly Gln Arg Arg Val	
180 185 190	
aat ggt gac tcc caa gca gta caa aaa tgt ttg att aca gaa tcc ccg	624
Asn Gly Asp Ser Gln Ala Val Gln Lys Cys Leu Ile Thr Glu Ser Pro	
195 200 205	
gca aag acc atg cag aga ctt gtc ccc cag cct gca gct aag gtc aca	672
Ala Lys Thr Met Gln Arg Leu Val Pro Gln Pro Ala Ala Lys Val Thr	
210 215 220	
cat cct gtt gat ccc cag tca gct gtt aag gtg cca gtt gga aga tcg	720
His Pro Val Asp Pro Gln Ser Ala Val Lys Val Pro Val Gly Arg Ser	
225 230 235 240	
ggc cta cct ctg aag tct tcg gga agt gtg gac cct tcg cct gct aga	768
Gly Leu Pro Leu Lys Ser Ser Gly Ser Val Asp Pro Ser Pro Ala Arg	
245 250 255	
gtt atg aga aga ttt gat cct cca cct gtt aag atg atg tca cag aga	816
Val Met Arg Arg Phe Asp Pro Pro Pro Val Lys Met Met Ser Gln Arg	
260 265 270	
gtt cac cat cca gct tcc atg gtg tcg cag aaa gtt gat cct ccg ttt	864
Val His His Pro Ala Ser Met Val Ser Gln Lys Val Asp Pro Pro Phe	
275 280 285	
ccg aag gta tta cat aag gaa acc gga tct gtt gtt cgc cta cca gaa	912
Pro Lys Val Leu His Lys Glu Thr Gly Ser Val Val Arg Leu Pro Glu	
290 295 300	
gct acc cgg cct act gtt ctt caa aaa ccc aag gac ttg cct gct atc	960
Ala Thr Arg Pro Thr Val Leu Gln Lys Pro Lys Asp Leu Pro Ala Ile	
305 310 315 320	
aag cag cag gat atc agg acc tct tcc tca aaa gaa gag ccc tgc ttc	1008
Lys Gln Gln Asp Ile Arg Thr Ser Ser Ser Lys Glu Glu Pro Cys Phe	

325	330	335	
tct ggt agg aat gca gaa gca gtt	caa gtg cag gat act aag ctc tcc		1056
Ser Gly Arg Asn Ala Glu Ala Val	Gln Val Gln Asp Thr Lys Leu Ser		
340	345	350	
cgg tca gay atg aag aaa atc cgc	aaa gct gag aaa aaa gat aag aag		1104
Arg Ser Asp Met Lys Lys Ile Arg	Lys Ala Glu Lys Lys Asp Lys Lys		
355	360	365	
ttc aga gat ctg ttt gtt acc tgg	aat ccg gta ttg ata gag aat gaa		1152
Phe Arg Asp Leu Phe Val Thr Trp	Asn Pro Val Leu Ile Glu Asn Glu		
370	375	380	
ggg tca gat ctt ggt gat gaa gac	tgg ctg ttc agc agt aaa agg aac		1200
Gly Ser Asp Leu Gly Asp Glu Asp	Trp Leu Phe Ser Ser Lys Arg Asn		
385	390	395	400
tcc gat gct atc atg gtt caa agc	aga gct act gat agt tca gtg ccg		1248
Ser Asp Ala Ile Met Val Gln Ser	Arg Ala Thr Asp Ser Ser Val Pro		
405	410	415	
atc cat cca atg gtg cag cag aag	cct tct tta caa ccc agg gca aca		1296
Ile His Pro Met Val Gln Gln Lys	Pro Ser Leu Gln Pro Arg Ala Thr		
420	425	430	
ttt ttg ccg gac ctt aat atg tac	cag ctg cca tat gtc gta cca ttt		1344
Phe Leu Pro Asp Leu Asn Met Tyr	Gln Leu Pro Tyr Val Val Pro Phe		
435	440	445	
taa			1347
<210> 48			
<211> 448			
<212> PRT			
<213> Zea mays mays strain Min13			
<400> 48			
Met Ser Arg Cys Phe Pro Tyr Pro	Pro Gly Tyr Val Arg Asn Pro		
1	5	10	15
Val Ala Val Ala Glu Pro Glu Ser	Thr Ala Lys Leu Leu Lys Glu Lys		
20	25	30	
Glu Lys Ala Glu Lys Lys Lys Glu	Lys Arg Ser Asp Arg Lys Ala Pro		
35	40	45	
Lys Gln Cys Glu Thr Ser Lys His	Ser Lys His Ser His Lys Lys Arg		
50	55	60	
Lys Leu Glu Asp Val Ile Lys Ala	Glu Gln Gly Pro Lys Arg Val Pro		

65

70

75

80

Lys Glu Ser Val Glu Gln Leu Glu Lys Ser Gly Leu Ser Glu Glu His
85 90 95

Gly Ala Pro Ser Phe Val His Thr Ile Arg Asp Ser Pro Glu Ser Ser
100 105 110

Gln Asp Ser Gly Lys Arg Arg Lys Val Val Leu Ser Ser Pro Ser Gln
115 120 125

Pro Lys Asn Gly Asn Ile Leu Arg Phe Lys Ile Lys Ser Ser Gln Asp
130 135 140

Pro Gln Ser Ala Val Leu Glu Lys Pro Arg Val Leu Glu Gln Pro Leu
145 150 155 160

Val Gln Gln Met Gly Ser Gly Ser Ser Leu Ser Gly Lys Gln Asn Ser
165 170 175

Ile His His Lys Met Asn Val Arg Ser Thr Ser Gly Gln Arg Arg Val
180 185 190

Asn Gly Asp Ser Gln Ala Val Gln Lys Cys Leu Ile Thr Glu Ser Pro
195 200 205

Ala Lys Thr Met Gln Arg Leu Val Pro Gln Pro Ala Ala Lys Val Thr
210 215 220

His Pro Val Asp Pro Gln Ser Ala Val Lys Val Pro Val Gly Arg Ser
225 230 235 240

Gly Leu Pro Leu Lys Ser Ser Gly Ser Val Asp Pro Ser Pro Ala Arg
245 250 255

Val Met Arg Arg Phe Asp Pro Pro Pro Val Lys Met Met Ser Gln Arg
260 265 270

Val His His Pro Ala Ser Met Val Ser Gln Lys Val Asp Pro Pro Phe
275 280 285

Pro Lys Val Leu His Lys Glu Thr Gly Ser Val Val Arg Leu Pro Glu
290 295 300

Ala Thr Arg Pro Thr Val Leu Gln Lys Pro Lys Asp Leu Pro Ala Ile
305 310 315 320

Lys Gln Gln Asp Ile Arg Thr Ser Ser Ser Lys Glu Glu Pro Cys Phe
325 330 335

Ser Gly Arg Asn Ala Glu Ala Val Gln Val Gln Asp Thr Lys Leu Ser
340 345 350

Arg Ser Asp Met Lys Lys Ile Arg Lys Ala Glu Lys Lys Asp Lys Lys
355 360 365

Phe Arg Asp Leu Phe Val Thr Trp Asn Pro Val Leu Ile Glu Asn Glu
370 375 380

Gly Ser Asp Leu Gly Asp Glu Asp Trp Leu Phe Ser Ser Lys Arg Asn
385 390 395 400

Ser Asp Ala Ile Met Val Gln Ser Arg Ala Thr Asp Ser Ser Val Pro
405 410 415

Ile His Pro Met Val Gln Gln Lys Pro Ser Leu Gln Pro Arg Ala Thr
420 425 430

Phe Leu Pro Asp Leu Asn Met Tyr Gln Leu Pro Tyr Val Val Pro Phe
435 440 445

<210> 49
<211> 495
<212> DNA
<213> Zea mays mays strain Pira

<400> 49
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ccttcggatt tacacacgca cgtgccagat cgttgttcaa tctgtagggt ttgcgcggat 180
ctgtggtttg cgcgtgcgtg atgtgggtat tgscctggcc ttgaaagcta accgagctga 240
ggaagtgtat ggatcttgtg tagctgcacg aggtcctcca aatcgattgt aaaatttaag 300
ttgtatggsc ggtaggsc aa gattgggtta gtccggtttt cgaaaactgg tagcatggtt 360
atcggggaca ttgaaagaat ggtagaacat caaattcgat tcaaaactgt gctagatttg 420

catatttagt cgccctaaaa ttacgtggac gtgggtgatc cgaattgggtt attgtatgat 480
 gggttggaata tgagc 495

<210> 50
 <211> 1768
 <212> DNA
 <213> Zea mays mays strain Pira

<400> 50
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 tttattgagc ccatttttag ttttcttggt ctgtagagta tgcattgttg caggctcttaa 120
 ctgttgtcag ggaagtaacg tgttcaacat gattgtaaac gaatacattc tgttgctaac 180
 tgtgtaatga tgagaaggat aattgaataa tctttgtgaa gtattactgt ctgaactgta 240
 cgcaatgcta cattcattct ttgtgttcgt gtaaataatca ttatacataa aaatgctgct 300
 tgcattcccg tcgtccgttc taaatcagaa ctgacgattg ctctgggtggc tgaagctcct 360
 gaaagaaaag gaaaaagccg aaaagaagaa agagaaaagg agtgacagga aagctcccaa 420
 gcagtgtgag acgtccaaac attcaaagca cagccataag aagagaaagc ttgaagatgt 480
 catcaaagct gagcagggtc caaaagagt acccaaagaa tcagttgagc agttggagaa 540
 gagtggactc tcagaagagc atggagctcc ttcttttgta catacgatac gtgactctcc 600
 tgagagctca caggacagcg gcaagagacg aaaggttgtc ctgtccagtc ctagccaacc 660
 taagaatggt gagactattc tottgttttt gctattctga ttgatttatt attatagaag 720
 aaatcaatca cttgttcagg attttattca tcccaacttg attttacagg aaacattctt 780
 cgcttcaaga ttaaaagtag tcaagatccc caatcagctg ttctggagaa accaagggtt 840
 cttgagcaac cattggtcca acaaattgga tcaggttcat ccctgtctgg caagcaaaat 900
 tcaatccatc ataagatgaa tgtgagatct acctctggtc agcggagggt caatggtgac 960
 tcccaagcag tacaaaaatg tttgattaca gaatccccgg caaagaccat gcagagactt 1020
 gtccccagc ctgcagctaa ggtcacacat cctgttgatc ccagtcagc tgtaaggtg 1080
 ccagttggaa gatcgggcct acctctgaag tcttcgggaa gtgtggacc ttcgcctgct 1140
 agagttatga gaagatttga tctccacct gttaagatga tgtcacagag agttcaccat 1200
 ccagcttcca tgggtgtcga gaaagttgat cctccgtttc cgaaggtatt acataaggaa 1260
 accggatctg ttgttcgcct accagaagct acccggccta ctgttcttca aaaaccaag 1320
 gacttgcctg ctatcaagca gcaggagatc aggacctctt yctcaaaaga agagccctgc 1380

2005-2006-2007

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ttctctggta ggaatgcaga agcagttcaa gtgcaggata ctaagctctc ccggtcagac 1440
atgaagaaaa tccgcaaagc tgagaaaaaa gataagaagt tcagagatct gtttgttacc 1500
tggaatccgg tattgataga gaatgaaggt tcagatcttg gtgatgaaga ctggctgttc 1560
agcagtaaaa ggaactccga tgctatcatg gttcaaagca gagctactga tagttcagtg 1620
ccgatccatc caatgggtgca gcagaagcct tctttacaac ccagggcaac atttttgccg 1680
gaccttaata tgtaccagct gccatatgtc gtaccatttt aaacatctgg cgaggtagat 1740
gagaattaga tgagatgttg ggagagag 1768

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<210> 51
<211> 1347
<212> DNA
<213> Zea mays mays strain Pira

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<220>
<221> CDS
<222> (1)..(1347)
<223>

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<400> 51
atg tcg agg tgc ttc ccc tac ccg cca ccg ggg tac gtg cgg aac cca 48
Met Ser Arg Cys Phe Pro Tyr Pro Pro Pro Gly Tyr Val Arg Asn Pro
1 5 10 15

gtg gcc gtg gcc gag ccg gag tcg acc gct aag ctc ctg aaa gaa aag 96
Val Ala Val Ala Glu Pro Glu Ser Thr Ala Lys Leu Leu Lys Glu Lys
20 25 30

gaa aaa gcc gaa aag aag aaa gag aaa agg agt gac agg aaa gct ccc 144
Glu Lys Ala Glu Lys Lys Lys Glu Lys Arg Ser Asp Arg Lys Ala Pro
35 40 45

aag cag tgt gag acg tcc aaa cat tca aag cac agc cat aag aag aga 192
Lys Gln Cys Glu Thr Ser Lys His Ser Lys His Ser His Lys Lys Arg
50 55 60

aag ctt gaa gat gtc atc aaa gct gag cag ggt ccc aaa aga gta ccc 240
Lys Leu Glu Asp Val Ile Lys Ala Glu Gln Gly Pro Lys Arg Val Pro
65 70 75 80

aaa gaa tca gtt gag cag ttg gag aag agt gga ctc tca gaa gag cat 288
Lys Glu Ser Val Glu Gln Leu Glu Lys Ser Gly Leu Ser Glu Glu His
85 90 95

gga gct cct tct ttt gta cat acg ata cgt gac tct cct gag agc tca 336
Gly Ala Pro Ser Phe Val His Thr Ile Arg Asp Ser Pro Glu Ser Ser
100 105 110

cag gac agc ggc aag aga cga aag gtt gtc ctg tcc agt cct agc caa 384

```

Gln Asp Ser Gly Lys Arg Arg Lys Val Val Leu Ser Ser Pro Ser Gln	
115 120 125	
cct aag aat gga aac att ctt cgc ttc aag att aaa agt agt caa gat	432
Pro Lys Asn Gly Asn Ile Leu Arg Phe Lys Ile Lys Ser Ser Gln Asp	
130 135 140	
ccc caa tca gct gtt ctg gag aaa cca agg gtt ctt gag caa cca ttg	480
Pro Gln Ser Ala Val Leu Glu Lys Pro Arg Val Leu Glu Gln Pro Leu	
145 150 155 160	
gtc caa caa atg gga tca ggt tca tcc ctg tct ggc aag caa aat tca	528
Val Gln Gln Met Gly Ser Gly Ser Ser Leu Ser Gly Lys Gln Asn Ser	
165 170 175	
atc cat cat aag atg aat gtg aga tct acc tct ggt cag cgg agg gtc	576
Ile His His Lys Met Asn Val Arg Ser Thr Ser Gly Gln Arg Arg Val	
180 185 190	
aat ggt gac tcc caa gca gta caa aaa tgt ttg att aca gaa tcc ccg	624
Asn Gly Asp Ser Gln Ala Val Gln Lys Cys Leu Ile Thr Glu Ser Pro	
195 200 205	
gca aag acc atg cag aga ctt gtc ccc cag cct gca gct aag gtc aca	672
Ala Lys Thr Met Gln Arg Leu Val Pro Gln Pro Ala Ala Lys Val Thr	
210 215 220	
cat cct gtt gat ccc cag tca gct gtt aag gtg cca gtt gga aga tcg	720
His Pro Val Asp Pro Gln Ser Ala Val Lys Val Pro Val Gly Arg Ser	
225 230 235 240	
ggc cta cct ctg aag tct tcg gga agt gtg gac cct tcg cct gct aga	768
Gly Leu Pro Leu Lys Ser Ser Gly Ser Val Asp Pro Ser Pro Ala Arg	
245 250 255	
gtt atg aga aga ttt gat cct cca cct gtt aag atg atg tca cag aga	816
Val Met Arg Arg Phe Asp Pro Pro Pro Val Lys Met Met Ser Gln Arg	
260 265 270	
gtt cac cat cca gct tcc atg gtg tcg cag aaa gtt gat cct ccg ttt	864
Val His His Pro Ala Ser Met Val Ser Gln Lys Val Asp Pro Pro Phe	
275 280 285	
ccg aag gta tta cat aag gaa acc gga tct gtt gtt cgc cta cca gaa	912
Pro Lys Val Leu His Lys Glu Thr Gly Ser Val Val Arg Leu Pro Glu	
290 295 300	
gct acc cgg cct act gtt ctt caa aaa ccc aag gac ttg cct gct atc	960
Ala Thr Arg Pro Thr Val Leu Gln Lys Pro Lys Asp Leu Pro Ala Ile	
305 310 315 320	
aag cag cag gag atc agg acc tct tyc tca aaa gaa gag ccc tgc ttc	1008
Lys Gln Gln Glu Ile Arg Thr Ser Xaa Ser Lys Glu Glu Pro Cys Phe	
325 330 335	
tct ggt agg aat gca gaa gca gtt caa gtg cag gat act aag ctc tcc	1056
Ser Gly Arg Asn Ala Glu Ala Val Gln Val Gln Asp Thr Lys Leu Ser	

205120" 2406400T

340	345	350	
cgg tca gac atg aag aaa atc cgc aaa gct gag aaa aaa gat aag aag Arg Ser Asp Met Lys Lys Ile Arg Lys Ala Glu Lys Lys Asp Lys Lys 355 360 365			1104
ttc aga gat ctg ttt gtt acc tgg aat ccg gta ttg ata gag aat gaa Phe Arg Asp Leu Phe Val Thr Trp Asn Pro Val Leu Ile Glu Asn Glu 370 375 380			1152
ggt tca gat ctt ggt gat gaa gac tgg ctg ttc agc agt aaa agg aac Gly Ser Asp Leu Gly Asp Glu Asp Trp Leu Phe Ser Ser Lys Arg Asn 385 390 395 400			1200
tcc gat gct atc atg gtt caa agc aga gct act gat agt tca gtg ccg Ser Asp Ala Ile Met Val Gln Ser Arg Ala Thr Asp Ser Ser Val Pro 405 410 415			1248
atc cat cca atg gtg cag cag aag cct tct tta caa ccc agg gca aca Ile His Pro Met Val Gln Gln Lys Pro Ser Leu Gln Pro Arg Ala Thr 420 425 430			1296
ttt ttg ccg gac ctt aat atg tac cag ctg cca tat gtc gta cca ttt Phe Leu Pro Asp Leu Asn Met Tyr Gln Leu Pro Tyr Val Val Pro Phe 435 440 445			1344
taa			1347

<210> 52
 <211> 448
 <212> PRT
 <213> Zea mays mays strain Pira
 <220>
 <221> misc_feature
 <222> (329)..(329)
 <223> The 'Xaa' at location 329 stands for Ser, or Phe.
 <400> 52

Met Ser Arg Cys Phe Pro Tyr Pro Pro Pro Gly Tyr Val Arg Asn Pro 1 5 10 15
Val Ala Val Ala Glu Pro Glu Ser Thr Ala Lys Leu Leu Lys Glu Lys 20 25 30
Glu Lys Ala Glu Lys Lys Lys Glu Lys Arg Ser Asp Arg Lys Ala Pro 35 40 45
Lys Gln Cys Glu Thr Ser Lys His Ser Lys His Ser His Lys Lys Arg 50 55 60

100704-0001

Lys Leu Glu Asp Val Ile Lys Ala Glu Gln Gly Pro Lys Arg Val Pro
65 70 75 80

Lys Glu Ser Val Glu Gln Leu Glu Lys Ser Gly Leu Ser Glu Glu His
85 90 95

Gly Ala Pro Ser Phe Val His Thr Ile Arg Asp Ser Pro Glu Ser Ser
100 105 110

Gln Asp Ser Gly Lys Arg Arg Lys Val Val Leu Ser Ser Pro Ser Gln
115 120 125

Pro Lys Asn Gly Asn Ile Leu Arg Phe Lys Ile Lys Ser Ser Gln Asp
130 135 140

Pro Gln Ser Ala Val Leu Glu Lys Pro Arg Val Leu Glu Gln Pro Leu
145 150 155 160

Val Gln Gln Met Gly Ser Gly Ser Ser Leu Ser Gly Lys Gln Asn Ser
165 170 175

Ile His His Lys Met Asn Val Arg Ser Thr Ser Gly Gln Arg Arg Val
180 185 190

Asn Gly Asp Ser Gln Ala Val Gln Lys Cys Leu Ile Thr Glu Ser Pro
195 200 205

Ala Lys Thr Met Gln Arg Leu Val Pro Gln Pro Ala Ala Lys Val Thr
210 215 220

His Pro Val Asp Pro Gln Ser Ala Val Lys Val Pro Val Gly Arg Ser
225 230 235 240

Gly Leu Pro Leu Lys Ser Ser Gly Ser Val Asp Pro Ser Pro Ala Arg
245 250 255

Val Met Arg Arg Phe Asp Pro Pro Pro Val Lys Met Met Ser Gln Arg
260 265 270

Val His His Pro Ala Ser Met Val Ser Gln Lys Val Asp Pro Pro Phe
275 280 285

Pro Lys Val Leu His Lys Glu Thr Gly Ser Val Val Arg Leu Pro Glu

290

295

300

Ala Thr Arg Pro Thr Val Leu Gln Lys Pro Lys Asp Leu Pro Ala Ile
305 310 315 320

Lys Gln Gln Glu Ile Arg Thr Ser Xaa Ser Lys Glu Glu Pro Cys Phe
325 330 335

Ser Gly Arg Asn Ala Glu Ala Val Gln Val Gln Asp Thr Lys Leu Ser
340 345 350

Arg Ser Asp Met Lys Lys Ile Arg Lys Ala Glu Lys Lys Asp Lys Lys
355 360 365

Phe Arg Asp Leu Phe Val Thr Trp Asn Pro Val Leu Ile Glu Asn Glu
370 375 380

Gly Ser Asp Leu Gly Asp Glu Asp Trp Leu Phe Ser Ser Lys Arg Asn
385 390 395 400

Ser Asp Ala Ile Met Val Gln Ser Arg Ala Thr Asp Ser Ser Val Pro
405 410 415

Ile His Pro Met Val Gln Gln Lys Pro Ser Leu Gln Pro Arg Ala Thr
420 425 430

Phe Leu Pro Asp Leu Asn Met Tyr Gln Leu Pro Tyr Val Val Pro Phe
435 440 445

<210> 53

<211> 212

<212> DNA

<213> Zea mays mays strain Sari

<400> 53

gcgcggtcga ccgtcggcat gtcgaggtgc ttcccctacc cgccaccggg gtacgtgcgg 60

aaccagtggt ccgtggccga gccggagtcg accgctaagg tttgttgaac cttcggattt 120

acacacgcac gtgccagatc gtttgttcaa tctgtaggtt ttgcgcggat ctgtggtttg 180

cgcggtgcgtg atgtgggtat tgcccgtgcc tt 212

<210> 54

<211> 1803

<212> DNA

<213> Zea mays mays strain Sari

<400> 54

ttttttcctt tttttttctg atgttactct tctgttgacc aaaggagttc agaattattt 60
tggccctgta tatcaatagc aaccaacacc atttattgag cccattttta gttttcttgt 120
tctgtagagt atgcattggt gcaggtctta actgttgtca gggaagtaac gtgttcaaca 180
tgattgtaaa cgaatacaat tctgttgcta actgtgtaat gatgagaagg ataattgaat 240
aatctttgtg aagtattact gtctgaactg tacgcaaag ctacattcat tctttgtgtt 300
cgtgtaaata tcattataca taaaaatgct gcattgcatt cccgtcgtcc gttctaaatc 360
agaactgacg attgctctgg tggtgaagc tcctgaaaga aaaggaaaag gccgaaaaga 420
agaaagagaa aaggagtgc aggaaagctc ccaagcagtg tgagacgtcc aaacattcaa 480
agcacagcca taagaagaga aagcttgaag atgtcatcaa agctgagcag ggccccaaaa 540
gagtacccaa agaatcagtt gagcagttgg agaagagtgg actctcagaa gagcatggag 600
ctccttcttt tgtacatacg atacgtgact ctcctgagag ctcacaggac agcggcaaga 660
gacgaaaggt tgtcctgtcc agtcctagcc aacctaagaa tggtagact attctcttgt 720
ttttgctatt ctgattgatt ttttattata gaagaaatca atcgcttgtt caggatttta 780
ttcatcccaa cttgatttta caggaaacat tcttcgcttc aagattaaaa gtagtcaaga 840
tccccaatca gctgttctgg agaaaccaag ggttcttgag caaccattgg tccaacaaat 900
gggatcaggt tcatccctgt cgggcaagca aaattcaatc catcataaga tgaatgtgag 960
atctacctct ggtcagcgga gggtaaatg tgactcccaa gcagtacaaa aatgtttgat 1020
tacagaatcc ccggcaaaga ccatgcagag acttggtccc cagcctgcag ctaaggtcac 1080
acatcctggt gatccccagt cagctgttaw ggtgccagtt ggaagatcgg gcctacctct 1140
gaagtcttcg ggaagtgtgg acccttcgcc tgctagagtt atgagaagat ttgatcctcc 1200
acctgttaag atgatgtcac agagagttca ccatccagct tccatggtgt cgcagaaagt 1260
tgatcctccg tttccgaagg tattacataa ggaaaccgga tctgttggtc gcctaccaga 1320
agctaccggy cctactgttc ttcaaaaacc caaggacttg cctgctatca agcagcagga 1380
tatcaggacc tcttcctcaa aagaagagcc ctgcttctct ggtaggaatg cagaagcagt 1440
tcaagtgcag gataactaagc tctcccggtc agayatgaag aaaatccgca aagctgagaa 1500
aaaagataag aagttcagag atctgtttgt tacctggaat ccggtattga tagagaatga 1560
aggttcagat cttggtgatg aagactggct gttcagcagt aaaaggaact ccgatgctat 1620

catggttcaa agcagagcta ctgatagttc agtgccgata catccaatgg tgcagcagaa 1680
gccttcttta caacccaggg caacattttt gccggacctt aatatgtacc agctgccata 1740
tgtcgtacca ttttaaacat ctggcgaggt agatgagaat tagatgagat gttgggagag 1800
agc 1803

<210> 55
<211> 1347
<212> DNA
<213> Zea mays mays strain Sari

<220>
<221> CDS
<222> (1)..(1347)
<223>

<400> 55
atg tgc agg tgc ttc ccc tac ccg cca ccg ggg tac gtg cgg aac cca 48
Met Ser Arg Cys Phe Pro Tyr Pro Pro Pro Gly Tyr Val Arg Asn Pro
1 5 10 15
gtg gcc gtg gcc gag ccg gag tgc acc gct aag ctc ctg aaa gaa aag 96
Val Ala Val Ala Glu Pro Glu Ser Thr Ala Lys Leu Leu Lys Glu Lys
20 25 30
gaa aag gcc gaa aag aag aaa gag aaa agg agt gac agg aaa gct ccc 144
Glu Lys Ala Glu Lys Lys Lys Glu Lys Arg Ser Asp Arg Lys Ala Pro
35 40 45
aag cag tgt gag acg tcc aaa cat tca aag cac agc cat aag aag aga 192
Lys Gln Cys Glu Thr Ser Lys His Ser Lys His Ser His Lys Lys Arg
50 55 60
aag ctt gaa gat gtc atc aaa gct gag cag ggt ccc aaa aga gta ccc 240
Lys Leu Glu Asp Val Ile Lys Ala Glu Gln Gly Pro Lys Arg Val Pro
65 70 75 80
aaa gaa tca gtt gag cag ttg gag aag agt gga ctc tca gaa gag cat 288
Lys Glu Ser Val Glu Gln Leu Glu Lys Ser Gly Leu Ser Glu Glu His
85 90 95
gga gct cct tct ttt gta cat acg ata cgt gac tct cct gag agc tca 336
Gly Ala Pro Ser Phe Val His Thr Ile Arg Asp Ser Pro Glu Ser Ser
100 105 110
cag gac agc gcc aag aga cga aag gtt gtc ctg tcc agt cct agc caa 384
Gln Asp Ser Gly Lys Arg Arg Lys Val Val Leu Ser Ser Pro Ser Gln
115 120 125
cct aag aat gga aac att ctt cgc ttc aag att aaa agt agt caa gat 432
Pro Lys Asn Gly Asn Ile Leu Arg Phe Lys Ile Lys Ser Ser Gln Asp
130 135 140

200604062001

ccc caa tca gct gtt ctg gag aaa cca agg gtt ctt gag caa cca ttg Pro Gln Ser Ala Val Leu Glu Lys Pro Arg Val Leu Glu Gln Pro Leu 145 150 155 160	480
gtc caa caa atg gga tca ggt tca tcc ctg tcg ggc aag caa aat tca Val Gln Gln Met Gly Ser Gly Ser Ser Leu Ser Gly Lys Gln Asn Ser 165 170 175	528
atc cat cat aag atg aat gtg aga tct acc tct ggt cag cgg agg gtc Ile His His Lys Met Asn Val Arg Ser Thr Ser Gly Gln Arg Arg Val 180 185 190	576
aat ggt gac tcc caa gca gta caa aaa tgt ttg att aca gaa tcc ccg Asn Gly Asp Ser Gln Ala Val Gln Lys Cys Leu Ile Thr Glu Ser Pro 195 200 205	624
gca aag acc atg cag aga ctt gtc ccc cag cct gca gct aag gtc aca Ala Lys Thr Met Gln Arg Leu Val Pro Gln Pro Ala Ala Lys Val Thr 210 215 220	672
cat cct gtt gat ccc cag tca gct gtt awg gtg cca gtt gga aga tcg His Pro Val Asp Pro Gln Ser Ala Val Xaa Val Pro Val Gly Arg Ser 225 230 235 240	720
ggc cta cct ctg aag tct tcg gga agt gtg gac cct tcg cct gct aga Gly Leu Pro Leu Lys Ser Ser Gly Ser Val Asp Pro Ser Pro Ala Arg 245 250 255	768
gtt atg aga aga ttt gat cct cca cct gtt aag atg atg tca cag aga Val Met Arg Arg Phe Asp Pro Pro Pro Val Lys Met Met Ser Gln Arg 260 265 270	816
gtt cac cat cca gct tcc atg gtg tcg cag aaa gtt gat cct ccg ttt Val His His Pro Ala Ser Met Val Ser Gln Lys Val Asp Pro Pro Phe 275 280 285	864
ccg aag gta tta cat aag gaa acc gga tct gtt gtt cgc cta cca gaa Pro Lys Val Leu His Lys Glu Thr Gly Ser Val Val Arg Leu Pro Glu 290 295 300	912
gct acc cgg cct act gtt ctt caa aaa ccc aag gac ttg cct gct atc Ala Thr Arg Pro Thr Val Leu Gln Lys Pro Lys Asp Leu Pro Ala Ile 305 310 315 320	960
aag cag cag gat atc agg acc tct tcc tca aaa gaa gag ccc tgc ttc Lys Gln Gln Asp Ile Arg Thr Ser Ser Ser Lys Glu Glu Pro Cys Phe 325 330 335	1008
tct ggt agg aat gca gaa gca gtt caa gtg car gat act aag ctc tcc Ser Gly Arg Asn Ala Glu Ala Val Gln Val Gln Asp Thr Lys Leu Ser 340 345 350	1056
cgg tca gay atg aag aaa atc cgc aaa gct gag aaa aaa gat aag aag Arg Ser Asp Met Lys Lys Ile Arg Lys Ala Glu Lys Lys Asp Lys Lys 355 360 365	1104
ttc aga gat ctg ttt gtt acc tgg aat ccg gta ttg ata gag aat gaa	1152

Phe Arg Asp Leu Phe Val Thr Trp Asn Pro Val Leu Ile Glu Asn Glu
 370 375 380

ggg tca gat ctt ggt gat gaa gac tgg ctg ttc agc agt aaa agg aac 1200
 Gly Ser Asp Leu Gly Asp Glu Asp Trp Leu Phe Ser Ser Lys Arg Asn
 385 390 395 400

tcc gat gct atc atg gtt caa agc aga gct act gat agt tca gtg ccg 1248
 Ser Asp Ala Ile Met Val Gln Ser Arg Ala Thr Asp Ser Ser Val Pro
 405 410 415

atc cat cca atg gtg cag cag aag cct tct tta caa ccc agg gca aca 1296
 Ile His Pro Met Val Gln Gln Lys Pro Ser Leu Gln Pro Arg Ala Thr
 420 425 430

ttt ttg ccg gac ctt aat atg tac cag ctg cca tat gtc gta cca ttt 1344
 Phe Leu Pro Asp Leu Asn Met Tyr Gln Leu Pro Tyr Val Val Pro Phe
 435 440 445

taa 1347

<210> 56
 <211> 448
 <212> PRT
 <213> Zea mays mays strain Sari
 <220>
 <221> misc_feature
 <222> (234)..(234)
 <223> The 'Xaa' at location 234 stands for Lys, or Met.

<400> 56

Met Ser Arg Cys Phe Pro Tyr Pro Pro Pro Gly Tyr Val Arg Asn Pro
 1 5 10 15

Val Ala Val Ala Glu Pro Glu Ser Thr Ala Lys Leu Leu Lys Glu Lys
 20 25 30

Glu Lys Ala Glu Lys Lys Lys Glu Lys Arg Ser Asp Arg Lys Ala Pro
 35 40 45

Lys Gln Cys Glu Thr Ser Lys His Ser Lys His Ser His Lys Lys Arg
 50 55 60

Lys Leu Glu Asp Val Ile Lys Ala Glu Gln Gly Pro Lys Arg Val Pro
 65 70 75 80

Lys Glu Ser Val Glu Gln Leu Glu Lys Ser Gly Leu Ser Glu Glu His
 85 90 95

206T00" 2405200T

Gly Ala Pro Ser Phe Val His Thr Ile Arg Asp Ser Pro Glu Ser Ser
100 105 110

Gln Asp Ser Gly Lys Arg Arg Lys Val Val Leu Ser Ser Pro Ser Gln
115 120 125

Pro Lys Asn Gly Asn Ile Leu Arg Phe Lys Ile Lys Ser Ser Gln Asp
130 135 140

Pro Gln Ser Ala Val Leu Glu Lys Pro Arg Val Leu Glu Gln Pro Leu
145 150 155 160

Val Gln Gln Met Gly Ser Gly Ser Ser Leu Ser Gly Lys Gln Asn Ser
165 170 175

Ile His His Lys Met Asn Val Arg Ser Thr Ser Gly Gln Arg Arg Val
180 185 190

Asn Gly Asp Ser Gln Ala Val Gln Lys Cys Leu Ile Thr Glu Ser Pro
195 200 205

Ala Lys Thr Met Gln Arg Leu Val Pro Gln Pro Ala Ala Lys Val Thr
210 215 220

His Pro Val Asp Pro Gln Ser Ala Val Xaa Val Pro Val Gly Arg Ser
225 230 235 240

Gly Leu Pro Leu Lys Ser Ser Gly Ser Val Asp Pro Ser Pro Ala Arg
245 250 255

Val Met Arg Arg Phe Asp Pro Pro Pro Val Lys Met Met Ser Gln Arg
260 265 270

Val His His Pro Ala Ser Met Val Ser Gln Lys Val Asp Pro Pro Phe
275 280 285

Pro Lys Val Leu His Lys Glu Thr Gly Ser Val Val Arg Leu Pro Glu
290 295 300

Ala Thr Arg Pro Thr Val Leu Gln Lys Pro Lys Asp Leu Pro Ala Ile
305 310 315 320

10079044-001900T

Lys Gln Gln Asp Ile Arg Thr Ser Ser Ser Lys Glu Glu Pro Cys Phe
325 330 335

Ser Gly Arg Asn Ala Glu Ala Val Gln Val Gln Asp Thr Lys Leu Ser
340 345 350

Arg Ser Asp Met Lys Lys Ile Arg Lys Ala Glu Lys Lys Asp Lys Lys
355 360 365

Phe Arg Asp Leu Phe Val Thr Trp Asn Pro Val Leu Ile Glu Asn Glu
370 375 380

Gly Ser Asp Leu Gly Asp Glu Asp Trp Leu Phe Ser Ser Lys Arg Asn
385 390 395 400

Ser Asp Ala Ile Met Val Gln Ser Arg Ala Thr Asp Ser Ser Val Pro
405 410 415

Ile His Pro Met Val Gln Gln Lys Pro Ser Leu Gln Pro Arg Ala Thr
420 425 430

Phe Leu Pro Asp Leu Asn Met Tyr Gln Leu Pro Tyr Val Val Pro Phe
435 440 445

<210> 57
<211> 305
<212> DNA
<213> Zea mays mays strain Smena

<400> 57
gattgatttc gagcgattcg attccttgtg atctctcggc ggggtagagc gcggtcgacc 60
gtcggccatg tcgaggtgct tcccctaccc gccaccgggg tacgtgcgga acccagtggc 120
cgtggccgag ccggagtcga ccgctaaggt ttgttgaacc ttcggattta cacacgcacg 180
tgccagatcg tttgttcaat atgtaggttt tgcgcggatc tgtggtttgc gcgtgcgtga 240
tgtgggtatt gcccgtcct aagctaaccg agctgaggaa gtgtatggat cttgtgtagc 300
tgcac 305

<210> 58
<211> 2208
<212> DNA
<213> Zea mays mays strain Smena

<400> 58

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ggaatatgag ccatctagtg cttccgtgac tggccaaatt tttttgtttc tcaaagtttt	120
ctttgaaaaa ctgtttgtcg agcgtcaatt cgtatttacc tgaatttact aattcttaat	180
acagtatgtc gttattttgg gctaagcttg tgtaagaagg gtcgtttgac attttgtact	240
gtattaatgc tgttttgtgt ttctttgttc ggagcagcat tcaatgctcc ttttgttggt	300
tgagagaatc tgatatttgc catcgtaccg aaagtccgaa accaactatt caaattggga	360
tttcatttct ttttttttct actgttttta gagttctctt tttcgtgct gtgctcttgt	420
gggtcagtac gtgcatttct ctcttttttt cttttttttt ctgatgttac tcttctgttg	480
accaaaggag ttcagaatta ttttggccct gtatatcaat ttgcaaccaa caccatttat	540
tgagcccatt ttagtttttc ttgttctgta gagttatgca ttgtttcagg tcttaactgt	600
tgtcagggaa gtaacgtggt caacatgatt gtaaacgaat acaattctgt tgctaactgt	660
gtaatgatga gaaggataat tgaatagtct ttgtgaagta ttactgtctg aactgtacgc	720
aaatgctaca ttcattctgt gttcatgtaa atatcattat acataaaaaat gctgcattgc	780
attcccgtcg tccgttctaa atcagaactg acgattgctc tgggtggctga agctcctgaa	840
agaaaaggaa aaggccgaaa agaagaaaga gaaaaggagt gacaggaaaag atcccaagca	900
gtgtgagacg tccaaacact caaagcacag ccataagaag agaaagcttg aagatgtcat	960
caaagctgag caggggtcca aaagagtacc caaagaatca gttgagcagt tggagaagag	1020
tggactctca gaagagcatg gagctccttc ttttgtacat acgatacggg actctcctga	1080
gagctcacag gacagcggca agagacgaaa ggttgtcctg tccagtccta gccaacctaa	1140
gaatggtgag actatttctt tgtttttgct attctgattg atttattatt atagaagaaa	1200
tcaatcaact gttcaggatt ttattcatcc caacttgatt ttacaggaaa cattcttcgc	1260
ttcaagatta aaagtagtca agatcccaa tcagctgttc tggagaaacc aagggttctt	1320
gagcaaccat tggccaaca aatgggatca gttcatccc tgtcgggcaa gcaaaattca	1380
atccatcata agatgaatgt gagatctacc tctggtcagc ggagggtcaa tggtgactcc	1440
caagcagtac aaaaatgttt gattacagaa tccccggcaa agaccatgca gagacttgtc	1500
ccccagcctg cagctaaggt cacacatcct gttgatcccc agtcagctgt taagggtcca	1560
gttggaagat cgggcctacc tctgaagtct tcaggaagtg tggacccttc gcctgctaga	1620
gttatgagaa gatttgatcc tccacctgtt aagatgatgt cacagagagt tcaccatcca	1680
gcttccatgg tgtcgcagaa agttgatcct ccgtttccga aggtattaca taaggaaacc	1740

ttatgagaag atttgatcct ccacctgtta agatgatgtc acagagagtt caccatccag 1080
 cttccatggg gtcgcagaaa gttgatcctc cgtttccgaa ggtattacat aaggaaaccg 1140
 gatctgttgt tcgcctacca gaagctaccc ggcctactgt tottcaaaaa cccaaggact 1200
 tgcctgctat caagcagcag gatatcagga cctcttctc aaaagaagag ccctgcttct 1260
 ctggtaggaa tgcagaagca gttcaagtgc aagatactaa gctctcccg tcagacatga 1320
 agaaaatccg caaagctgag aaaaaagata agaagttcag agatctgttt gttacctgga 1380
 atccgggtatt gatagagaat gaagggttcag atcttggtga tgaagactgg ctgttcagca 1440
 gtaaaaggaa ctccgatgct atcatgggtc aaagcagagc tactgatagt tcagtgccga 1500
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<220>
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 <222> (1)..(1347)
 <223>

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 Met Ser Arg Cys Phe Pro Tyr Pro Pro Pro Gly Tyr Val Arg Asn Pro
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 Val Ala Val Ala Glu Pro Glu Ser Thr Ala Lys Leu Leu Lys Glu Lys
 20 25 30
 gaa aag gcc gaa aag aag aaa gag aaa agg agt gac agg aaa gat ccc 144
 Glu Lys Ala Glu Lys Lys Lys Glu Lys Arg Ser Asp Arg Lys Asp Pro
 35 40 45
 aag cag tgt gag acg tcc aaa cac tca aag cac agc cat aag aag aga 192
 Lys Gln Cys Glu Thr Ser Lys His Ser Lys His Ser His Lys Lys Arg
 50 55 60
 aag ctt gaa gat gtc atc aaa gct gag cag ggt ccc aaa aga gta ccc 240
 Lys Leu Glu Asp Val Ile Lys Ala Glu Gln Gly Pro Lys Arg Val Pro
 65 70 75 80
 aaa gaa tca gtt gag cag ttg gag aag agt gga ctc tca gaa gag cat 288

Lys	Glu	Ser	Val	Glu	Gln	Leu	Glu	Lys	Ser	Gly	Leu	Ser	Glu	Glu	His	
			85						90					95		
gga	gct	cct	tct	ttt	gta	cat	acg	ata	cgg	gac	tct	cct	gag	agc	tca	336
Gly	Ala	Pro	Ser	Phe	Val	His	Thr	Ile	Arg	Asp	Ser	Pro	Glu	Ser	Ser	
			100					105					110			
cag	gac	agc	ggc	aag	aga	cga	aag	gtt	gtc	ctg	tcc	agt	cct	agc	caa	384
Gln	Asp	Ser	Gly	Lys	Arg	Arg	Lys	Val	Val	Leu	Ser	Ser	Pro	Ser	Gln	
			115				120					125				
cct	aag	aat	gga	aac	att	ctt	cgc	ttc	aag	att	aaa	agt	agt	caa	gat	432
Pro	Lys	Asn	Gly	Asn	Ile	Leu	Arg	Phe	Lys	Ile	Lys	Ser	Ser	Gln	Asp	
	130					135					140					
ccc	caa	tca	gct	gtt	ctg	gag	aaa	cca	agg	gtt	ctt	gag	caa	cca	ttg	480
Pro	Gln	Ser	Ala	Val	Leu	Glu	Lys	Pro	Arg	Val	Leu	Glu	Gln	Pro	Leu	
145					150				155						160	
gtc	caa	caa	atg	gga	tca	ggt	tca	tcc	ctg	tcg	ggc	aag	caa	aat	tca	528
Val	Gln	Gln	Met	Gly	Ser	Gly	Ser	Ser	Leu	Ser	Gly	Lys	Gln	Asn	Ser	
			165					170						175		
atc	cat	cat	aag	atg	aat	gtg	aga	tct	acc	tct	ggt	cag	cgg	agg	gtc	576
Ile	His	His	Lys	Met	Asn	Val	Arg	Ser	Thr	Ser	Gly	Gln	Arg	Arg	Val	
			180					185					190			
aat	ggt	gac	tcc	caa	gca	gta	caa	aaa	tgt	ttg	att	aca	gaa	tcc	ccg	624
Asn	Gly	Asp	Ser	Gln	Ala	Val	Gln	Lys	Cys	Leu	Ile	Thr	Glu	Ser	Pro	
		195					200					205				
gca	aag	acc	atg	cag	aga	ctt	gtc	ccc	cag	cct	gca	gct	aag	gtc	aca	672
Ala	Lys	Thr	Met	Gln	Arg	Leu	Val	Pro	Gln	Pro	Ala	Ala	Lys	Val	Thr	
	210					215					220					
cat	cct	gtt	gat	ccc	cag	tca	gct	gtt	aag	gtg	cca	gtt	gga	aga	tcg	720
His	Pro	Val	Asp	Pro	Gln	Ser	Ala	Val	Lys	Val	Pro	Val	Gly	Arg	Ser	
225					230				235						240	
ggc	cta	cct	ctg	aag	tct	tca	gga	agt	gtg	gac	cct	tcg	cct	gct	aga	768
Gly	Leu	Pro	Leu	Lys	Ser	Ser	Gly	Ser	Val	Asp	Pro	Ser	Pro	Ala	Arg	
				245					250					255		
gtt	atg	aga	aga	ttt	gat	cct	cca	cct	gtt	aag	atg	atg	tca	cag	aga	816
Val	Met	Arg	Arg	Phe	Asp	Pro	Pro	Pro	Val	Lys	Met	Met	Ser	Gln	Arg	
			260					265					270			
gtt	cac	cat	cca	gct	tcc	atg	gtg	tcg	cag	aaa	gtt	gat	cct	ccg	ttt	864
Val	His	His	Pro	Ala	Ser	Met	Val	Ser	Gln	Lys	Val	Asp	Pro	Pro	Phe	
		275					280					285				
ccg	aag	gta	tta	cat	aag	gaa	acc	gga	tct	gtt	gtt	cgc	cta	cca	gaa	912
Pro	Lys	Val	Leu	His	Lys	Glu	Thr	Gly	Ser	Val	Val	Arg	Leu	Pro	Glu	
	290					295					300					
gct	acc	cgg	cct	act	gtt	ctt	caa	aaa	ccc	aag	gac	ttg	cct	tct	atc	960
Ala	Thr	Arg	Pro	Thr	Val	Leu	Gln	Lys	Pro	Lys	Asp	Leu	Pro	Ser	Ile	

305	310	315	320	
aag cag cag gag atc agg acc tct tcc tca aaa gaa gag ccc tgc ttc				1008
Lys Gln Gln Glu Ile Arg Thr Ser Ser Ser Lys Glu Glu Pro Cys Phe				
325		330	335	
tct ggt agg aat gca gaa gct gtt caa gtg cag gat act aag ctc tcc				1056
Ser Gly Arg Asn Ala Glu Ala Val Gln Val Gln Asp Thr Lys Leu Ser				
340		345	350	
cgg tca gat atg aag aaa atc cgc aaa gct gag aaa aaa gat aag aag				1104
Arg Ser Asp Met Lys Lys Ile Arg Lys Ala Glu Lys Lys Asp Lys Lys				
355		360	365	
ttc aga gat ctg ttt gtt acc tgg aat ccg gta ttg ata gag aat gaa				1152
Phe Arg Asp Leu Phe Val Thr Trp Asn Pro Val Leu Ile Glu Asn Glu				
370		375	380	
ggt tca gat ctt ggt gat gaa gac tgg ctg ttc agc agt aaa agg aac				1200
Gly Ser Asp Leu Gly Asp Glu Asp Trp Leu Phe Ser Ser Lys Arg Asn				
385		390	395	400
tcc gat gct atc atg gtt caa agc aga gct act gat agt tca gtg ccg				1248
Ser Asp Ala Ile Met Val Gln Ser Arg Ala Thr Asp Ser Ser Val Pro				
405		410	415	
atc cat cca atg gtg cag cag aag cct tct tta caa ccc agg gca aca				1296
Ile His Pro Met Val Gln Gln Lys Pro Ser Leu Gln Pro Arg Ala Thr				
420		425	430	
ttt ttg ccg gac ctt aat atg tac cag ctg cca tat gtc gta cca ttt				1344
Phe Leu Pro Asp Leu Asn Met Tyr Gln Leu Pro Tyr Val Val Pro Phe				
435		440	445	
taa				1347
<210> 61				
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<212> PRT				
<213> Zea mays mays strain Smena				
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Met Ser Arg Cys Phe Pro Tyr Pro Pro Pro Gly Tyr Val Arg Asn Pro				
1 5 10 15				
Val Ala Val Ala Glu Pro Glu Ser Thr Ala Lys Leu Leu Lys Glu Lys				
20 25 30				
Glu Lys Ala Glu Lys Lys Lys Glu Lys Arg Ser Asp Arg Lys Asp Pro				
35 40 45				
Lys Gln Cys Glu Thr Ser Lys His Ser Lys His Ser His Lys Lys Arg				

50

55

60

Lys Leu Glu Asp Val Ile Lys Ala Glu Gln Gly Pro Lys Arg Val Pro
65 70 75 80

Lys Glu Ser Val Glu Gln Leu Glu Lys Ser Gly Leu Ser Glu Glu His
85 90 95

Gly Ala Pro Ser Phe Val His Thr Ile Arg Asp Ser Pro Glu Ser Ser
100 105 110

Gln Asp Ser Gly Lys Arg Arg Lys Val Val Leu Ser Ser Pro Ser Gln
115 120 125

Pro Lys Asn Gly Asn Ile Leu Arg Phe Lys Ile Lys Ser Ser Gln Asp
130 135 140

Pro Gln Ser Ala Val Leu Glu Lys Pro Arg Val Leu Glu Gln Pro Leu
145 150 155 160

Val Gln Gln Met Gly Ser Gly Ser Ser Leu Ser Gly Lys Gln Asn Ser
165 170 175

Ile His His Lys Met Asn Val Arg Ser Thr Ser Gly Gln Arg Arg Val
180 185 190

Asn Gly Asp Ser Gln Ala Val Gln Lys Cys Leu Ile Thr Glu Ser Pro
195 200 205

Ala Lys Thr Met Gln Arg Leu Val Pro Gln Pro Ala Ala Lys Val Thr
210 215 220

His Pro Val Asp Pro Gln Ser Ala Val Lys Val Pro Val Gly Arg Ser
225 230 235 240

Gly Leu Pro Leu Lys Ser Ser Gly Ser Val Asp Pro Ser Pro Ala Arg
245 250 255

Val Met Arg Arg Phe Asp Pro Pro Pro Val Lys Met Met Ser Gln Arg
260 265 270

Val His His Pro Ala Ser Met Val Ser Gln Lys Val Asp Pro Pro Phe
275 280 285

Pro Lys Val Leu His Lys Glu Thr Gly Ser Val Val Arg Leu Pro Glu
 290 295 300

Ala Thr Arg Pro Thr Val Leu Gln Lys Pro Lys Asp Leu Pro Ser Ile
 305 310 315 320

Lys Gln Gln Glu Ile Arg Thr Ser Ser Ser Lys Glu Glu Pro Cys Phe
 325 330 335

Ser Gly Arg Asn Ala Glu Ala Val Gln Val Gln Asp Thr Lys Leu Ser
 340 345 350

Arg Ser Asp Met Lys Lys Ile Arg Lys Ala Glu Lys Lys Asp Lys Lys
 355 360 365

Phe Arg Asp Leu Phe Val Thr Trp Asn Pro Val Leu Ile Glu Asn Glu
 370 375 380

Gly Ser Asp Leu Gly Asp Glu Asp Trp Leu Phe Ser Ser Lys Arg Asn
 385 390 395 400

Ser Asp Ala Ile Met Val Gln Ser Arg Ala Thr Asp Ser Ser Val Pro
 405 410 415

Ile His Pro Met Val Gln Gln Lys Pro Ser Leu Gln Pro Arg Ala Thr
 420 425 430

Phe Leu Pro Asp Leu Asn Met Tyr Gln Leu Pro Tyr Val Val Pro Phe
 435 440 445

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 <211> 893
 <212> DNA
 <213> Zea mays mays strain W22

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 tcgtttgttc aatctgtagg ttttgccgcg atctgtggtt tgcgcgtgcg tgatgtggcc 180
 ctgtgccttg aaagctaacc gagctgagga agtgtatgga tcttgtgtag ctgcacgagg 240
 tcctccaaat cgattgtaaa atttaagttg tatggccggg aggccaagat tgggttagtc 300

cggttttcga aaactggtag catggttatc ggggacattg aaagaatggt agaacaatcaa 360
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 ggtgatccga attggttggt gtatgatggt tggaagtgcac tggccaaatt tttttgtttc 480
 tcaaagtttt ctttgaaaaa ctgtttgtcg agcgtcaatt cgtattttacc tgaattttact 540
 aattcttaat acagtatttc gttatttttcg gctaagcttg tgtaagaagg gtcgtttgac 600
 attttgtact gtattaatgc tgttttgtgt ttctttgttc ggagcagcat tcaatgctcc 660
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 caaattggga ttccatttct tttttctact gtttttagag ttctcttttt cgctgctgtg 780
 ctcttggtggg tcagtacgtg cattttctctt tttttttctg atgttactct tctgttgacc 840
 aaaggagtgc agaattattt tggccctgta tatcaatagc aaccaacacc att 893

<210> 63
 <211> 1411
 <212> DNA
 <213> Zea mays mays strain W22

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 gatgtcatca aagctgagca ggggtccaaa agagtaccca aagaatcagt tgagcagttg 180
 gagaagagtg gactctcaga agagcatgga gctccttctt ttgtacatac gatacgtgac 240
 tctcctgaga gctcacagga cagcggcaag agacgaaagg ttgtcctgtc cagtcctagc 300
 caacctaaaga atggtgagac tattctcttg tttttgctat tctgattgat tttttattat 360
 agaagaaatc aatcgcttgt tcaggatttt attcatccca acttgatttt acaggaaaca 420
 ttcttcgctt caagattaaa agtagtcaag accccaatc agctgttctg gagaaaccaa 480
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 aaaattcaat ccatcataag atgaatgtga gatctacctc tggtcagcgg agggtcgatg 600
 gtgactccca agcagtacaa aaatggttga ttacagaatc cccggcaaag accatgcaga 660
 gacttgtooc ccagcctgca gctaagggtca cacatcctgt tgatccccag tcagctgtta 720
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 ctgctagagt tatgagaaga tttgatcctc cacctgttaa gatgatgtca cagagagttc 840
 accatccagc ttccatggtg tcgcagaaag ttgatcctcc gtttccgaag gtattacata 900

aggaaaccgg atctgttggt cgcctaccag aagctacccg gcctactggt cttcaaaaac 960
 ccaaggactt gcctgctatc aagcagcagg atatcaggac ctcttcctca aaagaagagc 1020
 cctgcttctc tggtaggaat gcagaagcag ttcaagtgca agataactaag ctctcccggg 1080
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 tggtcagcag taaaaggaac tccgatgcta tcatggttca aagcagagct actgatagtt 1260
 cagtgccgat ccaccaatg gtgcagcaga agccttcttt acaaccagg gcaacatttt 1320
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 tagatagaat tagatagatg ttggggagaga g 1411

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 <212> DNA
 <213> Zea mays mays strain W22

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<400> 64
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 Val Ala Val Ala Glu Pro Glu Ser Thr Ala Lys Leu Leu Lys Glu Lys
 20 25 30
 gaa aag gcc gaa aag aag aaa gag aaa agg agt gac agg aaa gct ccc 144
 Glu Lys Ala Glu Lys Lys Lys Glu Lys Arg Ser Asp Arg Lys Ala Pro
 35 40 45
 aag cag tgt gag acg tcc aaa cat tca aag cac agc cat aag aag aga 192
 Lys Gln Cys Glu Thr Ser Lys His Ser Lys His Ser His Lys Lys Arg
 50 55 60
 aag ctt gaa gat gtc atc aaa gct gag cag ggt ccc aaa aga gta ccc 240
 Lys Leu Glu Asp Val Ile Lys Ala Glu Gln Gly Pro Lys Arg Val Pro
 65 70 75 80
 aaa gaa tca gtt gag cag ttg gag aag agt gga ctc tca gaa gag cat 288
 Lys Glu Ser Val Glu Gln Leu Glu Lys Ser Gly Leu Ser Glu Glu His
 85 90 95
 gga gct cct tct ttt gta cat acg ata cgt gac tct cct gag agc tca 336

Gly	Ala	Pro	Ser	Phe	Val	His	Thr	Ile	Arg	Asp	Ser	Pro	Glu	Ser	Ser		
		100						105					110				
cag	gac	agc	ggc	aag	aga	cga	aag	gtt	gtc	ctg	tcc	agt	cct	agc	caa		384
Gln	Asp	Ser	Gly	Lys	Arg	Arg	Lys	Val	Val	Leu	Ser	Ser	Pro	Ser	Gln		
		115					120					125					
cct	aag	aat	gga	aac	att	ctt	cgc	ttc	aag	att	aaa	agt	agt	caa	gac		432
Pro	Lys	Asn	Gly	Asn	Ile	Leu	Arg	Phe	Lys	Ile	Lys	Ser	Ser	Ser	Gln	Asp	
		130				135					140						
ccc	caa	tca	gct	gtt	ctg	gag	aaa	cca	agg	gtt	ctt	gag	caa	cca	ttg		480
Pro	Gln	Ser	Ala	Val	Leu	Glu	Lys	Pro	Arg	Val	Leu	Glu	Gln	Pro	Leu		
		145			150				155						160		
gtc	caa	caa	atg	gga	tca	ggt	tca	tcc	ccg	tcg	ggc	aag	caa	aat	tca		528
Val	Gln	Gln	Met	Gly	Ser	Gly	Ser	Ser	Pro	Ser	Gly	Lys	Gln	Asn	Ser		
				165					170					175			
atc	cat	cat	aag	atg	aat	gtg	aga	tct	acc	tct	ggt	cag	cgg	agg	gtc		576
Ile	His	His	Lys	Met	Asn	Val	Arg	Ser	Thr	Ser	Gly	Gln	Arg	Arg	Val		
			180					185					190				
gat	ggt	gac	tcc	caa	gca	gta	caa	aaa	tgt	ttg	att	aca	gaa	tcc	ccg		624
Asp	Gly	Asp	Ser	Gln	Ala	Val	Gln	Lys	Cys	Leu	Ile	Thr	Glu	Ser	Pro		
		195					200					205					
gca	aag	acc	atg	cag	aga	ctt	gtc	ccc	cag	cct	gca	gct	aag	gtc	aca		672
Ala	Lys	Thr	Met	Gln	Arg	Leu	Val	Pro	Gln	Pro	Ala	Ala	Lys	Val	Thr		
		210				215					220						
cat	cct	gtt	gat	ccc	cag	tca	gct	gtt	aag	gtg	cca	gtt	gga	aga	tcg		720
His	Pro	Val	Asp	Pro	Gln	Ser	Ala	Val	Lys	Val	Pro	Val	Gly	Arg	Ser		
		225			230				235						240		
ggc	cta	cct	ctg	aag	tct	tcg	gga	agt	gtg	gac	cct	tcg	cct	gct	aga		768
Gly	Leu	Pro	Leu	Lys	Ser	Ser	Gly	Ser	Val	Asp	Pro	Ser	Pro	Ala	Arg		
				245					250					255			
gtt	atg	aga	aga	ttt	gat	cct	cca	cct	gtt	aag	atg	atg	tca	cag	aga		816
Val	Met	Arg	Arg	Phe	Asp	Pro	Pro	Pro	Val	Lys	Met	Met	Ser	Gln	Arg		
				260				265					270				
gtt	cac	cat	cca	gct	tcc	atg	gtg	tcg	cag	aaa	gtt	gat	cct	ccg	ttt		864
Val	His	His	Pro	Ala	Ser	Met	Val	Ser	Gln	Lys	Val	Asp	Pro	Pro	Phe		
		275					280					285					
ccg	aag	gta	tta	cat	aag	gaa	acc	gga	tct	gtt	gtt	cgc	cta	cca	gaa		912
Pro	Lys	Val	Leu	His	Lys	Glu	Thr	Gly	Ser	Val	Val	Arg	Leu	Pro	Glu		
		290				295					300						
gct	acc	cgg	cct	act	gtt	ctt	caa	aaa	ccc	aag	gac	ttg	cct	gct	atc		960
Ala	Thr	Arg	Pro	Thr	Val	Leu	Gln	Lys	Pro	Lys	Asp	Leu	Pro	Ala	Ile		
		305			310				315						320		
aag	cag	cag	gat	atc	agg	acc	tct	tcc	tca	aaa	gaa	gag	ccc	tgc	ttc		1008
Lys	Gln	Gln	Asp	Ile	Arg	Thr	Ser	Ser	Ser	Lys	Glu	Glu	Pro	Cys	Phe		

325	330	335	
tct ggt agg aat gca gaa gca gtt caa gtg caa gat act aag ctc tcc			1056
Ser Gly Arg Asn Ala Glu Ala Val Gln Val Gln Asp Thr Lys Leu Ser			
340	345	350	
cgg tca gac atg aag aaa atc cgc aaa gct gag aaa aaa gat aag aag			1104
Arg Ser Asp Met Lys Lys Ile Arg Lys Ala Glu Lys Lys Asp Lys Lys			
355	360	365	
ttc aga gat ctg ttt gtt acc tgg aat ccg gta ttg ata gag aat gaa			1152
Phe Arg Asp Leu Phe Val Thr Trp Asn Pro Val Leu Ile Glu Asn Glu			
370	375	380	
ggg tca gat ctt ggt gat gaa gac tgg ctg ttc agc agt aaa agg aac			1200
Gly Ser Asp Leu Gly Asp Glu Asp Trp Leu Phe Ser Ser Lys Arg Asn			
385	390	400	
tcc gat gct atc atg gtt caa agc aga gct act gat agt tca gtg ccg			1248
Ser Asp Ala Ile Met Val Gln Ser Arg Ala Thr Asp Ser Ser Val Pro			
405	410	415	
atc cat cca atg gtg cag cag aag cct tct tta caa ccc agg gca aca			1296
Ile His Pro Met Val Gln Gln Lys Pro Ser Leu Gln Pro Arg Ala Thr			
420	425	430	
ttt ttg ccg gac ctt aat atg tac cag ctg cca tat gtc gta cca ttt			1344
Phe Leu Pro Asp Leu Asn Met Tyr Gln Leu Pro Tyr Val Val Pro Phe			
435	440	445	
taa			1347
<210> 65			
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<400> 65			
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Val Ala Val Ala Glu Pro Glu Ser Thr Ala Lys Leu Leu Lys Glu Lys			
20	25	30	
Glu Lys Ala Glu Lys Lys Lys Glu Lys Arg Ser Asp Arg Lys Ala Pro			
35	40	45	
Lys Gln Cys Glu Thr Ser Lys His Ser Lys His Ser His Lys Lys Arg			
50	55	60	
Lys Leu Glu Asp Val Ile Lys Ala Glu Gln Gly Pro Lys Arg Val Pro			

65

70

75

80

Lys Glu Ser Val Glu Gln Leu Glu Lys Ser Gly Leu Ser Glu Glu His
85 90 95

Gly Ala Pro Ser Phe Val His Thr Ile Arg Asp Ser Pro Glu Ser Ser
100 105 110

Gln Asp Ser Gly Lys Arg Arg Lys Val Val Leu Ser Ser Pro Ser Gln
115 120 125

Pro Lys Asn Gly Asn Ile Leu Arg Phe Lys Ile Lys Ser Ser Gln Asp
130 135 140

Pro Gln Ser Ala Val Leu Glu Lys Pro Arg Val Leu Glu Gln Pro Leu
145 150 155 160

Val Gln Gln Met Gly Ser Gly Ser Ser Pro Ser Gly Lys Gln Asn Ser
165 170 175

Ile His His Lys Met Asn Val Arg Ser Thr Ser Gly Gln Arg Arg Val
180 185 190

Asp Gly Asp Ser Gln Ala Val Gln Lys Cys Leu Ile Thr Glu Ser Pro
195 200 205

Ala Lys Thr Met Gln Arg Leu Val Pro Gln Pro Ala Ala Lys Val Thr
210 215 220

His Pro Val Asp Pro Gln Ser Ala Val Lys Val Pro Val Gly Arg Ser
225 230 235 240

Gly Leu Pro Leu Lys Ser Ser Gly Ser Val Asp Pro Ser Pro Ala Arg
245 250 255

Val Met Arg Arg Phe Asp Pro Pro Pro Val Lys Met Met Ser Gln Arg
260 265 270

Val His His Pro Ala Ser Met Val Ser Gln Lys Val Asp Pro Pro Phe
275 280 285

Pro Lys Val Leu His Lys Glu Thr Gly Ser Val Val Arg Leu Pro Glu
290 295 300

Ala Thr Arg Pro Thr Val Leu Gln Lys Pro Lys Asp Leu Pro Ala Ile
305 310 315 320

Lys Gln Gln Asp Ile Arg Thr Ser Ser Ser Lys Glu Glu Pro Cys Phe
325 330 335

Ser Gly Arg Asn Ala Glu Ala Val Gln Val Gln Asp Thr Lys Leu Ser
340 345 350

Arg Ser Asp Met Lys Lys Ile Arg Lys Ala Glu Lys Lys Asp Lys Lys
355 360 365

Phe Arg Asp Leu Phe Val Thr Trp Asn Pro Val Leu Ile Glu Asn Glu
370 375 380

Gly Ser Asp Leu Gly Asp Glu Asp Trp Leu Phe Ser Ser Lys Arg Asn
385 390 395 400

Ser Asp Ala Ile Met Val Gln Ser Arg Ala Thr Asp Ser Ser Val Pro
405 410 415

Ile His Pro Met Val Gln Gln Lys Pro Ser Leu Gln Pro Arg Ala Thr
420 425 430

Phe Leu Pro Asp Leu Asn Met Tyr Gln Leu Pro Tyr Val Val Pro Phe
435 440 445

<210> 66
<211> 2644
<212> DNA
<213> Zea mays parviglumis strain Benz

<400> 66
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tcgtttgttc aatctgtagg ttttgcgcg atctgtggtt tgcgcgtgcg tgatgtgggt 180
attgcccggt ccttgaaagc taaccgagct gaggaagtgt atggatcttg ttagctgca 240
cgaggtcctc caaatcgatt gtaaaattta agttgtatgg ccggtaggcc aagattgggt 300
tattccggtt ttcgaaaact ggtagcatgg ttatcgggga cattgaaaga atggtagaac 360
atcaaattcg attcaaaact gtgctagatt tgcattatcta gtcgccctaa aattacgtgg 420

acgtgggtga tccgaattgg ttgttgtatg atggttggaa gtgactggcc aaatTTTTTT	480
gtttctcaaa gttttctttg acaaactggt tgctgagcgt caattcgtat ttacctgaat	540
ttactaattc ttaatacagt atgtcgttat tttgggctaa gcttgtgtaa gaagggctgt	600
ttgacatttt gtactgtatt gatgctgttt tgtgtttctt tgttcggagc agcattcaat	660
gctccttttg ttgtttgaga gaatctgata tttgccatcg taccgaaagt ccgaaaccaa	720
ctattcaaat tgggatttca tttctTTTTT ttctactggt tttagagttc tctttttcgc	780
tgctgtgctc ttgtgggtca gtacgtgcat ttctctTTTT ttctTTTTTT ttctgatgtt	840
actcttctgt tgaccaaagg agttcagaat tattttggcc ctgtatatca atagcaacca	900
acaccattta ttgagcccat ttttagtttt cttgttctgt agagtatgca ttgttgcagg	960
tcttaactgt tgtcagggaa gtaacgtggt caacatgatt gtaaacgaat acaattctgt	1020
tgctaaactgt gtaatgatga gaaggataat tgaataatct ttgtgaagta ttactgtctg	1080
aactgtacgc aaatgctaca ttcattcttt gtgttcgtgt aaatatcatt atacataaaa	1140
atgtctgatt gcattcccggt cgtccgttct aaatcagaac tgacgattgc tctggtggct	1200
gaagctcctg aaagaaaagg aaaaggccga aaagaagaaa gagaaaagga gtgacaggaa	1260
agctcccaag cagtgtgaga cgtccaaaca ttcaaagcac agccataaga agagaaagct	1320
tgaagatgtc atcaaagctg agcaggggtc caaaagagta ccaaagaat cagttgagca	1380
gttgaggaaag agtggactct cagaagagca tggagctcct tcttttgtac atacgatacg	1440
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ttatagaaga aatcaatcgc ttgttcagga ttttattcat cccaactga ttttacagga	1620
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aatggtgact cccaagcagt acaaaaatgt ttgattacag aatccccggc aaagaccatg	1860
cagagacttg tccccagcc tgcagctaag gtcacacatc ctgttgatcc ccagtcagct	1920
gttaaggtgc cagttggaag atcgggccta cctctgaagt cttcggaag tgtggaccct	1980
tcgcctgcta gagttatgag aagatttgat cctccacctg ttaagatgat gtcacagaga	2040
gttcaccatc cagcttccat ggtgtcgag aaagttgatc ctccgtttcc gaaggtatta	2100

cataaggaaa ccg gatctgt tgttcgccta ccagaagcta cccggcctac tgttcttcaa 2160
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gagccctgct tctctggtag gaatgcagaa gcagttcaag tgcaagatac taagctctcc 2280
cggtcagaca tgaagaaaat ccgcaaagct gagaaaaaag ataagaagtt cagagatctg 2340
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tggctgttca gcagtaaaaag gaactccgat gctatcatgg ttcaaagcag agctactgat 2460
agttcagtgc cgatccatcc aatgggtgcag cagaagcctt ctttacaacc cagggcaaca 2520
tttttgccgg accttaatat gtaccagctg ccatatgtcg taccatttta aacatctggc 2580
gaggtagatg agaattagat gagatgttgg gagagagctg tgtgaacagt aggccgggta 2640
gctt 2644

<210> 67
<211> 1347
<212> DNA
<213> Zea mays parviglumis strain Benz

<220>
<221> CDS
<222> (1)..(1347)
<223>

<400> 67
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Met Ser Arg Cys Phe Pro Tyr Pro Pro Pro Gly Tyr Val Arg Asn Pro
1 5 10 15
gtg gcc gtg gcc gag ccg gag tcg acc gct aag ctc ctg aaa gaa aag 96
Val Ala Val Ala Glu Pro Glu Ser Thr Ala Lys Leu Leu Lys Glu Lys
20 25 30
gaa aag gcc gaa aag aag aaa gag aaa agg agt gac agg aaa gct ccc 144
Glu Lys Ala Glu Lys Lys Lys Glu Lys Arg Ser Asp Arg Lys Ala Pro
35 40 45
aag cag tgt gag acg tcc aaa cat tca aag cac agc cat aag aag aga 192
Lys Gln Cys Glu Thr Ser Lys His Ser Lys His Ser His Lys Lys Arg
50 55 60
aag ctt gaa gat gtc atc aaa gct gag cag ggt ccc aaa aga gta ccc 240
Lys Leu Glu Asp Val Ile Lys Ala Glu Gln Gly Pro Lys Arg Val Pro
65 70 75 80
aaa gaa tca gtt gag cag ttg gag aag agt gga ctc tca gaa gag cat 288
Lys Glu Ser Val Glu Gln Leu Glu Lys Ser Gly Leu Ser Glu Glu His
85 90 95

gga gct cct tct ttt gta cat acg ata cgt gac tct cct gag agc tca	336
Gly Ala Pro Ser Phe Val His Thr Ile Arg Asp Ser Pro Glu Ser Ser	
100 105 110	
cag gac agc ggc aag aga cga aag gtt gtc ctg tcc agt cct agc caa	384
Gln Asp Ser Gly Lys Arg Arg Lys Val Val Leu Ser Ser Pro Ser Gln	
115 120 125	
cct aag aat gga aac att ctt cgc ttc aag att aaa agt agt caa gat	432
Pro Lys Asn Gly Asn Ile Leu Arg Phe Lys Ile Lys Ser Ser Gln Asp	
130 135 140	
ccc caa tca gct gtt ctg gag aaa cca agg gtt ctt gag caa cca ttg	480
Pro Gln Ser Ala Val Leu Glu Lys Pro Arg Val Leu Glu Gln Pro Leu	
145 150 155 160	
gtc caa caa atg gga tca ggt tca tcc ctg tgc ggc aag caa aat tca	528
Val Gln Gln Met Gly Ser Gly Ser Ser Leu Ser Gly Lys Gln Asn Ser	
165 170 175	
atc cat cat aag atg aat gtg aga tct acc tct ggt cag cgg agg gtc	576
Ile His His Lys Met Asn Val Arg Ser Thr Ser Gly Gln Arg Arg Val	
180 185 190	
aat ggt gac tcc caa gca gta caa aaa tgt ttg att aca gaa tcc ccg	624
Asn Gly Asp Ser Gln Ala Val Gln Lys Cys Leu Ile Thr Glu Ser Pro	
195 200 205	
gca aag acc atg cag aga ctt gtc ccc cag cct gca gct aag gtc aca	672
Ala Lys Thr Met Gln Arg Leu Val Pro Gln Pro Ala Ala Lys Val Thr	
210 215 220	
cat cct gtt gat ccc cag tca gct gtt aag gtg cca gtt gga aga tcg	720
His Pro Val Asp Pro Gln Ser Ala Val Lys Val Pro Val Gly Arg Ser	
225 230 235 240	
ggc cta cct ctg aag tct tgc gga agt gtg gac cct tgc cct gct aga	768
Gly Leu Pro Leu Lys Ser Ser Gly Ser Val Asp Pro Ser Pro Ala Arg	
245 250 255	
gtt atg aga aga ttt gat cct cca cct gtt aag atg atg tca cag aga	816
Val Met Arg Arg Phe Asp Pro Pro Pro Val Lys Met Met Ser Gln Arg	
260 265 270	
gtt cac cat cca gct tcc atg gtg tgc cag aaa gtt gat cct ccg ttt	864
Val His His Pro Ala Ser Met Val Ser Gln Lys Val Asp Pro Pro Phe	
275 280 285	
ccg aag gta tta cat aag gaa acc gga tct gtt gtt cgc cta cca gaa	912
Pro Lys Val Leu His Lys Glu Thr Gly Ser Val Val Arg Leu Pro Glu	
290 295 300	
gct acc cgg cct act gtt ctt caa aaa ccc aag gac ttg cct gct atc	960
Ala Thr Arg Pro Thr Val Leu Gln Lys Pro Lys Asp Leu Pro Ala Ile	
305 310 315 320	
aag cag cag gat atc agg acc tct tcc tca aaa gaa gag ccc tgc ttc	1008

206720" 2405400T

Lys Gln Gln Asp Ile Arg Thr Ser Ser Ser Lys Glu Glu Pro Cys Phe
325 330 335

tct ggt agg aat gca gaa gca gtt caa gtg caa gat act aag ctc tcc 1056
Ser Gly Arg Asn Ala Glu Ala Val Gln Val Gln Asp Thr Lys Leu Ser
340 345 350

cgg tca gac atg aag aaa atc cgc aaa gct gag aaa aaa gat aag aag 1104
Arg Ser Asp Met Lys Lys Ile Arg Lys Ala Glu Lys Lys Asp Lys Lys
355 360 365

ttc aga gat ctg ttt gtt acc tgg aat ccg gta ttg ata gag aat gaa 1152
Phe Arg Asp Leu Phe Val Thr Trp Asn Pro Val Leu Ile Glu Asn Glu
370 375 380

ggg tca gat ctt ggt gat gaa gac tgg ctg ttc agc agt aaa agg aac 1200
Gly Ser Asp Leu Gly Asp Glu Asp Trp Leu Phe Ser Ser Lys Arg Asn
385 390 395 400

tcc gat gct atc atg gtt caa agc aga gct act gat agt tca gtg ccg 1248
Ser Asp Ala Ile Met Val Gln Ser Arg Ala Thr Asp Ser Ser Val Pro
405 410 415

atc cat cca atg gtg cag cag aag cct tct tta caa ccc agg gca aca 1296
Ile His Pro Met Val Gln Gln Lys Pro Ser Leu Gln Pro Arg Ala Thr
420 425 430

ttt ttg ccg gac ctt aat atg tac cag ctg cca tat gtc gta cca ttt 1344
Phe Leu Pro Asp Leu Asn Met Tyr Gln Leu Pro Tyr Val Val Pro Phe
435 440 445

taa 1347

<210> 68

<211> 448

<212> PRT

<213> Zea mays parviglumis strain Benz

<400> 68

Met Ser Arg Cys Phe Pro Tyr Pro Pro Pro Gly Tyr Val Arg Asn Pro
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Val Ala Val Ala Glu Pro Glu Ser Thr Ala Lys Leu Leu Lys Glu Lys
20 25 30

Glu Lys Ala Glu Lys Lys Lys Glu Lys Arg Ser Asp Arg Lys Ala Pro
35 40 45

Lys Gln Cys Glu Thr Ser Lys His Ser Lys His Ser His Lys Lys Arg
50 55 60

Lys Leu Glu Asp Val Ile Lys Ala Glu Gln Gly Pro Lys Arg Val Pro
65 70 75 80

Lys Glu Ser Val Glu Gln Leu Glu Lys Ser Gly Leu Ser Glu Glu His
85 90 95

Gly Ala Pro Ser Phe Val His Thr Ile Arg Asp Ser Pro Glu Ser Ser
100 105 110

Gln Asp Ser Gly Lys Arg Arg Lys Val Val Leu Ser Ser Pro Ser Gln
115 120 125

Pro Lys Asn Gly Asn Ile Leu Arg Phe Lys Ile Lys Ser Ser Gln Asp
130 135 140

Pro Gln Ser Ala Val Leu Glu Lys Pro Arg Val Leu Glu Gln Pro Leu
145 150 155 160

Val Gln Gln Met Gly Ser Gly Ser Ser Leu Ser Gly Lys Gln Asn Ser
165 170 175

Ile His His Lys Met Asn Val Arg Ser Thr Ser Gly Gln Arg Arg Val
180 185 190

Asn Gly Asp Ser Gln Ala Val Gln Lys Cys Leu Ile Thr Glu Ser Pro
195 200 205

Ala Lys Thr Met Gln Arg Leu Val Pro Gln Pro Ala Ala Lys Val Thr
210 215 220

His Pro Val Asp Pro Gln Ser Ala Val Lys Val Pro Val Gly Arg Ser
225 230 235 240

Gly Leu Pro Leu Lys Ser Ser Gly Ser Val Asp Pro Ser Pro Ala Arg
245 250 255

Val Met Arg Arg Phe Asp Pro Pro Pro Val Lys Met Met Ser Gln Arg
260 265 270

Val His His Pro Ala Ser Met Val Ser Gln Lys Val Asp Pro Pro Phe
275 280 285

Pro Lys Val Leu His Lys Glu Thr Gly Ser Val Val Arg Leu Pro Glu

290

295

300

Ala Thr Arg Pro Thr Val Leu Gln Lys Pro Lys Asp Leu Pro Ala Ile
 305 310 315 320

Lys Gln Gln Asp Ile Arg Thr Ser Ser Ser Lys Glu Glu Pro Cys Phe
 325 330 335

Ser Gly Arg Asn Ala Glu Ala Val Gln Val Gln Asp Thr Lys Leu Ser
 340 345 350

Arg Ser Asp Met Lys Lys Ile Arg Lys Ala Glu Lys Lys Asp Lys Lys
 355 360 365

Phe Arg Asp Leu Phe Val Thr Trp Asn Pro Val Leu Ile Glu Asn Glu
 370 375 380

Gly Ser Asp Leu Gly Asp Glu Asp Trp Leu Phe Ser Ser Lys Arg Asn
 385 390 395 400

Ser Asp Ala Ile Met Val Gln Ser Arg Ala Thr Asp Ser Ser Val Pro
 405 410 415

Ile His Pro Met Val Gln Gln Lys Pro Ser Leu Gln Pro Arg Ala Thr
 420 425 430

Phe Leu Pro Asp Leu Asn Met Tyr Gln Leu Pro Tyr Val Val Pro Phe
 435 440 445

<210> 69

<211> 586

<212> DNA

<213> Zea mays parviglumis strain BK4

<400> 69

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cgtgccagat cgtttgttca atctgtaggt tttgcgcgga tctgtggttt gcgcgtgcgt 180

gatgtggccc gtgccttgaa agctaaccga gctgaggaag tgtatggatc ttgtgtagct 240

gcacgaggtc ctccaaatcg attgtaaaat ttaagttgta tggccggtag gccaagattg 300

ggttagtccg gttttcgaaa actggtagca tggttatcgg ggacattgaa agaatggtag 360

aacatcaaat tcgattcaaa actgtgctag atttgcataat ttagtcgccc taaaattacg	420
tggacgtggg tgatccgaat tggttgttgt atgatggttg gaagtgactg gccaaatddd	480
ttgtttctca aagttttctt tgaaaaactg tttgtcgagc gtcaattcgt atttacctga	540
atttactaat tcttaataca gtatttcggt attttcgggt aagctt	586

<210> 70
 <211> 1775
 <212> DNA
 <213> Zea mays parviglumis strain BK4

<400> 70	
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accatttatt gatcccattd ttagttttct tgttctgtag agtatgcatt gttgcaggtc	120
ttaactgttg tcaggaagt aacgtgttca acatgattgt aaacgaatac aattctgttg	180
ctaactgtgt aatgatgaga aggataattg aataatcttd gtgaagtatt actgtctgaa	240
ctgtacgcaa atgctacatt cattctttgt gttcgtgtaa atatcattat acataaaaaat	300
gctgcattgc attcccgtcg tccgttctaa tcagaactga cgattgctct ggtggctgaa	360
gctcctgaaa gaaaaggaaa aggccgaaaa gaagaaagag aaaaggagtg acaggaaagc	420
tccaagcag tgtgagacgt ccaaacattc aaagcacagc cataagaaga gaaagcttga	480
agatgtcatc aaagctgagc agggccccaa aagagtacc c aaagaatcag ttgagcagtt	540
ggagaagagt ggactctcag aagagcatgg agctccttct tttgtacata cgatacgtga	600
ctctcctgag agctcacagg acagcggcaa gagacgaaag gttgtcctgt ccagtcctag	660
ccaacctaag aatggtgaga ctattctctt gtttttgcta ttctgattga tttttatta	720
tagaagaaat caatcgcttg ttcaggattt tattcatccc aacttgattt tacaggaaac	780
attcttcgct tcaagattaa aagtagtcaa gacccccaat cagctgttct ggagaaacca	840
agggttcttg agcaaccatt ggtccaacaa atgggatcag gttcatcccc gtcgggcaag	900
caaaattcaa tccatcataa gatgaatgtg agatctacct ctggtcagcg gaggtcagat	960
ggtgactccc aagcagtaca aaaatgtttg attacagaat ccccgcaaa gaccatgcag	1020
agacttgtcc cccagcctgc agctaaggtc acacatcctg ttgatcccca gtcagctgtt	1080
aagggtccag ttggaagatc gggcctacct ctgaagtctt cgggaagtgt ggacccttcg	1140
cctgctagag ttatgagaag atttgatcct ccacctgtta agatgatgtc acagagagtt	1200
caccatccag cttocatggg gtcgcagaaa gttgatcctc cgtttccgaa ggtattacat	1260

aaggaaaccg gatctgttgt tcgcctacca gaagctaccc ggcctactgt tcttcaaaaa 1320
 cccaaggact tgcttgctat caagcagcag gatatcagga cctcttctctc aaaagaagag 1380
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 tcagacatga agaaaatccg caaagctgag aaaaaagata agaagttcag agatctgttt 1500
 gttacctgga atccggtatt gatagagaat gaaggttcag atcttggtga tgaagactgg 1560
 ctgttcagca gtaaaaggaa ctccgatgct atcatggttc aaagcagagc tactgatagt 1620
 tcagtgccga tccatccaat ggtgcagcag aagccttctt tacaaccag ggcaacattt 1680
 ttgccggacc ttaatatgta ccagctgcc aatgtcgtag cattttaaac atctggcgag 1740
 gtagatgaga attagatgag atgttgggag agagc 1775

<210> 71
 <211> 1347
 <212> DNA
 <213> Zea mays parviglumis strain BK4

<220>
 <221> CDS
 <222> (1)..(1347)
 <223>

<400> 71
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 gtg gcc gtg gcc gag ccg gag tcg acc gct aag ctc ctg aaa gaa aag 96
 Val Ala Val Ala Glu Pro Glu Ser Thr Ala Lys Leu Leu Lys Glu Lys
 20 25 30
 gaa aag gcc gaa aag aag aaa gag aaa agg agt gac agg aaa gct ccc 144
 Glu Lys Ala Glu Lys Lys Lys Glu Lys Arg Ser Asp Arg Lys Ala Pro
 35 40 45
 aag cag tgt gag acg tcc aaa cat tca aag cac agc cat aag aag aga 192
 Lys Gln Cys Glu Thr Ser Lys His Ser Lys His Ser His Lys Lys Arg
 50 55 60
 aag ctt gaa gat gtc atc aaa gct gag cag ggt ccc aaa aga gta ccc 240
 Lys Leu Glu Asp Val Ile Lys Ala Glu Gln Gly Pro Lys Arg Val Pro
 65 70 75 80
 aaa gaa tca gtt gag cag ttg gag aag agt gga ctc tca gaa gag cat 288
 Lys Glu Ser Val Glu Gln Leu Glu Lys Ser Gly Leu Ser Glu Glu His
 85 90 95
 gga gct cct tct ttt gta cat acg ata cgt gac tct cct gag agc tca 336
 Gly Ala Pro Ser Phe Val His Thr Ile Arg Asp Ser Pro Glu Ser Ser

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cag gac agc ggc aag aga cga aag gtt gtc ctg tcc agt cct agc caa				384
Gln Asp Ser Gly Lys Arg Arg Lys Val Val Leu Ser Ser Pro Ser Gln	115	120	125	
cct aag aat gga aac att ctt cgc ttc aag att aaa agt agt caa gac				432
Pro Lys Asn Gly Asn Ile Leu Arg Phe Lys Ile Lys Ser Ser Gln Asp	130	135	140	
ccc caa tca gct gtt ctg gag aaa cca agg gtt ctt gag caa cca ttg				480
Pro Gln Ser Ala Val Leu Glu Lys Pro Arg Val Leu Glu Gln Pro Leu	145	150	155	160
gtc caa caa atg gga tca ggt tca tcc ccg tcg ggc aag caa aat tca				528
Val Gln Gln Met Gly Ser Gly Ser Ser Pro Ser Gly Lys Gln Asn Ser	165	170	175	
atc cat cat aag atg aat gtg aga tct acc tct ggt cag cgg agg gtc				576
Ile His His Lys Met Asn Val Arg Ser Thr Ser Gly Gln Arg Arg Val	180	185	190	
gat ggt gac tcc caa gca gta caa aaa tgt ttg att aca gaa tcc ccg				624
Asp Gly Asp Ser Gln Ala Val Gln Lys Cys Leu Ile Thr Glu Ser Pro	195	200	205	
gca aag acc atg cag aga ctt gtc ccc cag cct gca gct aag gtc aca				672
Ala Lys Thr Met Gln Arg Leu Val Pro Gln Pro Ala Ala Lys Val Thr	210	215	220	
cat cct gtt gat ccc cag tca gct gtt aag gtg cca gtt gga aga tcg				720
His Pro Val Asp Pro Gln Ser Ala Val Lys Val Pro Val Gly Arg Ser	225	230	235	240
ggc cta cct ctg aag tct tcg gga agt gtg gac cct tcg cct gct aga				768
Gly Leu Pro Leu Lys Ser Ser Gly Ser Val Asp Pro Ser Pro Ala Arg	245	250	255	
gtt atg aga aga ttt gat cct cca cct gtt aag atg atg tca cag aga				816
Val Met Arg Arg Phe Asp Pro Pro Pro Val Lys Met Met Ser Gln Arg	260	265	270	
gtt cac cat cca gct tcc atg gtg tcg cag aaa gtt gat cct ccg ttt				864
Val His His Pro Ala Ser Met Val Ser Gln Lys Val Asp Pro Pro Phe	275	280	285	
ccg aag gta tta cat aag gaa acc gga tct gtt gtt cgc cta cca gaa				912
Pro Lys Val Leu His Lys Glu Thr Gly Ser Val Val Arg Leu Pro Glu	290	295	300	
gct acc cgg cct act gtt ctt caa aaa ccc aag gac ttg cct gct atc				960
Ala Thr Arg Pro Thr Val Leu Gln Lys Pro Lys Asp Leu Pro Ala Ile	305	310	315	320
aag cag cag gat atc agg acc tct tcc tca aaa gaa gag ccc tgc ttc				1008
Lys Gln Gln Asp Ile Arg Thr Ser Ser Ser Lys Glu Glu Pro Cys Phe	325	330	335	

tct ggt agg aat gca gaa gca gtt caa gtg caa gat act aag ctc tcc 1056
Ser Gly Arg Asn Ala Glu Ala Val Gln Val Gln Asp Thr Lys Leu Ser
340 345 350

cgg tca gac atg aag aaa atc cgc aaa gct gag aaa aaa gat aag aag 1104
Arg Ser Asp Met Lys Lys Ile Arg Lys Ala Glu Lys Lys Asp Lys Lys
355 360 365

ttc aga gat ctg ttt gtt acc tgg aat ccg gta ttg ata gag aat gaa 1152
Phe Arg Asp Leu Phe Val Thr Trp Asn Pro Val Leu Ile Glu Asn Glu
370 375 380

ggt tca gat ctt ggt gat gaa gac tgg ctg ttc agc agt aaa agg aac 1200
Gly Ser Asp Leu Gly Asp Glu Asp Trp Leu Phe Ser Ser Lys Arg Asn
385 390 395 400

tcc gat gct atc atg gtt caa agc aga gct act gat agt tca gtg ccg 1248
Ser Asp Ala Ile Met Val Gln Ser Arg Ala Thr Asp Ser Ser Val Pro
405 410 415

atc cat cca atg gtg cag cag aag cct tct tta caa ccc agg gca aca 1296
Ile His Pro Met Val Gln Gln Lys Pro Ser Leu Gln Pro Arg Ala Thr
420 425 430

ttt ttg ccg gac ctt aat atg tac cag ctg cca tat gtc gta cca ttt 1344
Phe Leu Pro Asp Leu Asn Met Tyr Gln Leu Pro Tyr Val Val Pro Phe
435 440 445

taa 1347

<210> 72
<211> 448
<212> PRT
<213> Zea mays parviglumis strain BK4

<400> 72

Met Ser Arg Cys Phe Pro Tyr Pro Pro Pro Gly Tyr Val Arg Asn Pro
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Val Ala Val Ala Glu Pro Glu Ser Thr Ala Lys Leu Leu Lys Glu Lys
20 25 30

Glu Lys Ala Glu Lys Lys Lys Glu Lys Arg Ser Asp Arg Lys Ala Pro
35 40 45

Lys Gln Cys Glu Thr Ser Lys His Ser Lys His Ser His Lys Lys Arg
50 55 60

Lys Leu Glu Asp Val Ile Lys Ala Glu Gln Gly Pro Lys Arg Val Pro
65 70 75 80

Lys Glu Ser Val Glu Gln Leu Glu Lys Ser Gly Leu Ser Glu Glu His
85 90 95

Gly Ala Pro Ser Phe Val His Thr Ile Arg Asp Ser Pro Glu Ser Ser
100 105 110

Gln Asp Ser Gly Lys Arg Arg Lys Val Val Leu Ser Ser Pro Ser Gln
115 120 125

Pro Lys Asn Gly Asn Ile Leu Arg Phe Lys Ile Lys Ser Ser Gln Asp
130 135 140

Pro Gln Ser Ala Val Leu Glu Lys Pro Arg Val Leu Glu Gln Pro Leu
145 150 155 160

Val Gln Gln Met Gly Ser Gly Ser Ser Pro Ser Gly Lys Gln Asn Ser
165 170 175

Ile His His Lys Met Asn Val Arg Ser Thr Ser Gly Gln Arg Arg Val
180 185 190

Asp Gly Asp Ser Gln Ala Val Gln Lys Cys Leu Ile Thr Glu Ser Pro
195 200 205

Ala Lys Thr Met Gln Arg Leu Val Pro Gln Pro Ala Ala Lys Val Thr
210 215 220

His Pro Val Asp Pro Gln Ser Ala Val Lys Val Pro Val Gly Arg Ser
225 230 235 240

Gly Leu Pro Leu Lys Ser Ser Gly Ser Val Asp Pro Ser Pro Ala Arg
245 250 255

Val Met Arg Arg Phe Asp Pro Pro Pro Val Lys Met Met Ser Gln Arg
260 265 270

Val His His Pro Ala Ser Met Val Ser Gln Lys Val Asp Pro Pro Phe
275 280 285

Pro Lys Val Leu His Lys Glu Thr Gly Ser Val Val Arg Leu Pro Glu
290 295 300

Ala Thr Arg Pro Thr Val Leu Gln Lys Pro Lys Asp Leu Pro Ala Ile
305 310 315 320

Lys Gln Gln Asp Ile Arg Thr Ser Ser Ser Lys Glu Glu Pro Cys Phe
325 330 335

Ser Gly Arg Asn Ala Glu Ala Val Gln Val Gln Asp Thr Lys Leu Ser
340 345 350

Arg Ser Asp Met Lys Lys Ile Arg Lys Ala Glu Lys Lys Asp Lys Lys
355 360 365

Phe Arg Asp Leu Phe Val Thr Trp Asn Pro Val Leu Ile Glu Asn Glu
370 375 380

Gly Ser Asp Leu Gly Asp Glu Asp Trp Leu Phe Ser Ser Lys Arg Asn
385 390 395 400

Ser Asp Ala Ile Met Val Gln Ser Arg Ala Thr Asp Ser Ser Val Pro
405 410 415

Ile His Pro Met Val Gln Gln Lys Pro Ser Leu Gln Pro Arg Ala Thr
420 425 430

Phe Leu Pro Asp Leu Asn Met Tyr Gln Leu Pro Tyr Val Val Pro Phe
435 440 445

<210> 73

<211> 305

<212> DNA

<213> Zea mays parviglumis strain IA19

<400> 73

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cgtcggccat gtcgaggtgc ttcccctacc cgccaccggg gtacgtgcgg aaccagtggt 120

ccgtggccga gccggagtcg accgctaagg tttgttgaac cttcggattt acacacgcac 180

gtgccagatc gtttgttcaa tctgtaggtt ttgcgcggat ctgtgggtttg cgcgtgcgtg 240

atgtgggtat tgcccgtgcc ttgaaagcta accgagctga ggaagtgtat ggatcttgtg 300

tagct 305

<210> 74

<211> 1309
 <212> DNA
 <213> Zea mays parviglumis strain IA19

<400> 74

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ggagctcctt cttttgtaca tacgatacgt gactctcctg agagctcaca ggacagcggc	180
aagagacgaa aggttgtcct gtccagtcct agccaaccta agaatggtga gactattctc	240
ttgtttttgc tattctgatt gattttttat tatagaagaa atcaatcgct tgttcaggat	300
tttattcatc ccaacttgat ttacaggaa acattcttctg cttcaagatt aaaagtagtc	360
aagatcccca atcagctgtt ctggagaaac caagggttct tgagcaacca ttggtccaac	420
aatgggatc aggttcatcc ctgtcgggca agcaaaattc aatccatcat aagatgaatg	480
tgagatctac ctctggtcag cggaggggtca atgggtgactc ccaagcagta caaaaatgtt	540
tgattacaga atccccggca aagaccatgc agagacttgt cccccagcct gcagctaagg	600
tcacacatcc tgttgatccc cagtcagctg ttaaggtgcc agttggaaga tcgggcctac	660
ctctgaagtc ttcgggaagt gtggaccctt cgctgctag agttatgaga agatttgatc	720
ctccacctgt taagatgatg tcacagagag ttcaccatcc agcttccatg gtgtcgcaga	780
aagttgatcc tccgtttccg aaggtattac ataaggaaac cggatctgtt gttcgcctac	840
cagaagctac ccggcctact gttctttcaa aacccaagga cttgcctgct atcaagcagc	900
aggakatcag gacctcttcc tcaaaagaag agccctgctt ctctggtagg aatgcagaag	960
cagttcaagt gcaggatact aagctctccc ggtcagacat gaagaaaatc cgcaaagctg	1020
agaaaaaaga taagaagttc agagatctgt ttgttacctg gaatccggtg ttgatagaga	1080
atgaaggttc agatcttggt gatgaagact ggctgttcag cagtaaaagg aactccgatg	1140
ctatcatggt tcaaagcaga gctactgata gttcagtgcc gatccatcca atgggtgcagc	1200
agaagccttc tttaacaacc agggcaacat ttttgccgga ccttaatatg taccagctgc	1260
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<210> 75
 <211> 1347
 <212> DNA
 <213> Zea mays parviglumis strain IA19

<220>
 <221> CDS

<222> (1)..(1332)
 <223>

<220>
 <221> misc_feature
 <222> (82)..(168)
 <223> n = A, C, T, or G

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 1 5 10 15

gtg gcc gtg gcc gag ccg gag tcg acc gct aag nnn nnn nnn nnn nnn 96
 Val Ala Val Ala Glu Pro Glu Ser Thr Ala Lys Xaa Xaa Xaa Xaa Xaa
 20 25 30

nnn nnn nnn nnn nnn nnn nnn nnn nnn nnn nnn nnn nnn nnn nnn 144
 Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
 35 40 45

nnn nnn nnn nnn nnn nnn nnn nnn tca aag cac agc cat aag aag aga 192
 Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Ser Lys His Ser His Lys Lys Arg
 50 55 60

aag ctt gaa gat gtc atc aaa gct gag cag gtt ccc aaa aga gta ccc 240
 Lys Leu Glu Asp Val Ile Lys Ala Glu Gln Val Pro Lys Arg Val Pro
 65 70 75 80

aaa gaa tca gtt gag cag ttg gag aag agt gga ctc tca gaa gag cat 288
 Lys Glu Ser Val Glu Gln Leu Glu Lys Ser Gly Leu Ser Glu Glu His
 85 90 95

gga gct cct tct ttt gta cat acg ata cgt gac tct cct gag agc tca 336
 Gly Ala Pro Ser Phe Val His Thr Ile Arg Asp Ser Pro Glu Ser Ser
 100 105 110

cag gac agc ggc aag aga cga aag gtt gtc ctg tcc agt cct agc caa 384
 Gln Asp Ser Gly Lys Arg Arg Lys Val Val Leu Ser Ser Pro Ser Gln
 115 120 125

cct aag aat gga aac att ctt cgc ttc aag att aaa agt agt caa gat 432
 Pro Lys Asn Gly Asn Ile Leu Arg Phe Lys Ile Lys Ser Ser Gln Asp
 130 135 140

ccc caa tca gct gtt ctg gag aaa cca agg gtt ctt gag caa cca ttg 480
 Pro Gln Ser Ala Val Leu Glu Lys Pro Arg Val Leu Glu Gln Pro Leu
 145 150 155 160

gtc caa caa atg gga tca ggt tca tcc ctg tcg ggc aag caa aat tca 528
 Val Gln Gln Met Gly Ser Gly Ser Ser Leu Ser Gly Lys Gln Asn Ser
 165 170 175

atc cat cat aag atg aat gtg aga tct acc tct ggt cag cgg agg gtc 576
 Ile His His Lys Met Asn Val Arg Ser Thr Ser Gly Gln Arg Arg Val

180	185	190	
aat ggt gac tcc caa gca gta caa aaa tgt ttg att aca gaa tcc ccg Asn Gly Asp Ser Gln Ala Val Gln Lys Cys Leu Ile Thr Glu Ser Pro 195 200 205			624
gca aag acc atg cag aga ctt gtc ccc cag cct gca gct aag gtc aca Ala Lys Thr Met Gln Arg Leu Val Pro Gln Pro Ala Ala Lys Val Thr 210 215 220			672
cat cct gtt gat ccc cag tca gct gtt aag gtg cca gtt gga aga tcg His Pro Val Asp Pro Gln Ser Ala Val Lys Val Pro Val Gly Arg Ser 225 230 235 240			720
ggc cta cct ctg aag tct tcg gga agt gtg gac cct tcg cct gct aga Gly Leu Pro Leu Lys Ser Ser Gly Ser Val Asp Pro Ser Pro Ala Arg 245 250 255			768
gtt atg aga aga ttt gat cct cca cct gtt aag atg atg tca cag aga Val Met Arg Arg Phe Asp Pro Pro Pro Val Lys Met Met Ser Gln Arg 260 265 270			816
gtt cac cat cca gct tcc atg gtg tcg cag aaa gtt gat cct ccg ttt Val His His Pro Ala Ser Met Val Ser Gln Lys Val Asp Pro Pro Phe 275 280 285			864
ccg aag gta tta cat aag gaa acc gga tct gtt gtt cgc cta cca gaa Pro Lys Val Leu His Lys Glu Thr Gly Ser Val Val Arg Leu Pro Glu 290 295 300			912
gct acc cgg cct act gtt ctt caa aaa ccc aag gac ttg cct gct atc Ala Thr Arg Pro Thr Val Leu Gln Lys Pro Lys Asp Leu Pro Ala Ile 305 310 315 320			960
aag cag cag gak atc agg acc tct tcc tca aaa gaa gag ccc tgc ttc Lys Gln Gln Xaa Ile Arg Thr Ser Ser Ser Lys Glu Glu Pro Cys Phe 325 330 335			1008
tct ggt agg aat gca gaa gca gtt caa gtg cag gat act aag ctc tcc Ser Gly Arg Asn Ala Glu Ala Val Gln Val Gln Asp Thr Lys Leu Ser 340 345 350			1056
cgg tca gac atg aag aaa atc cgc aaa gct gag aaa aaa gat aag aag Arg Ser Asp Met Lys Lys Ile Arg Lys Ala Glu Lys Lys Asp Lys Lys 355 360 365			1104
ttc aga gat ctg ttt gtt acc tgg aat ccg gta ttg ata gag aat gaa Phe Arg Asp Leu Phe Val Thr Trp Asn Pro Val Leu Ile Glu Asn Glu 370 375 380			1152
ggt tca gat ctt ggt gat gaa gac tgg ctg ttc agc agt aaa agg aac Gly Ser Asp Leu Gly Asp Glu Asp Trp Leu Phe Ser Ser Lys Arg Asn 385 390 395 400			1200
tcc gat gct atc atg gtt caa agc aga gct act gat agt tca gtg ccg Ser Asp Ala Ile Met Val Gln Ser Arg Ala Thr Asp Ser Ser Val Pro 405 410 415			1248

atc cat cca atg gtg cag cag aag cct tct tta caa ccc agg gca aca 1296
 Ile His Pro Met Val Gln Gln Lys Pro Ser Leu Gln Pro Arg Ala Thr
 420 425 430

ttt ttg ccg gac ctt aat atg tac cag ctg cca tat gtcgtacccat tttaa 1347
 Phe Leu Pro Asp Leu Asn Met Tyr Gln Leu Pro Tyr
 435 440

<210> 76
 <211> 444
 <212> PRT
 <213> Zea mays parviglumis strain IA19

<220>
 <221> misc_feature
 <222> (28)..(28)
 <223> The 'Xaa' at location 28 stands for Lys, Asn, Arg, Ser, Thr, Ile,
 Met, Glu, Asp, Gly, Ala, Val, Gln, His, Pro, Leu, a stop codon,
 Tyr, Trp, Cys, or Phe.

<220>
 <221> misc_feature
 <222> (29)..(29)
 <223> The 'Xaa' at location 29 stands for Lys, Asn, Arg, Ser, Thr, Ile,
 Met, Glu, Asp, Gly, Ala, Val, Gln, His, Pro, Leu, a stop codon,
 Tyr, Trp, Cys, or Phe.

<220>
 <221> misc_feature
 <222> (30)..(30)
 <223> The 'Xaa' at location 30 stands for Lys, Asn, Arg, Ser, Thr, Ile,
 Met, Glu, Asp, Gly, Ala, Val, Gln, His, Pro, Leu, a stop codon,
 Tyr, Trp, Cys, or Phe.

<220>
 <221> misc_feature
 <222> (31)..(31)
 <223> The 'Xaa' at location 31 stands for Lys, Asn, Arg, Ser, Thr, Ile,
 Met, Glu, Asp, Gly, Ala, Val, Gln, His, Pro, Leu, a stop codon,
 Tyr, Trp, Cys, or Phe.

<220>
 <221> misc_feature
 <222> (32)..(32)
 <223> The 'Xaa' at location 32 stands for Lys, Asn, Arg, Ser, Thr, Ile,
 Met, Glu, Asp, Gly, Ala, Val, Gln, His, Pro, Leu, a stop codon,
 Tyr, Trp, Cys, or Phe.

<220>
 <221> misc_feature
 <222> (33)..(33)
 <223> The 'Xaa' at location 33 stands for Lys, Asn, Arg, Ser, Thr, Ile,
 Met, Glu, Asp, Gly, Ala, Val, Gln, His, Pro, Leu, a stop codon,
 Tyr, Trp, Cys, or Phe.

<220>
<221> misc_feature
<222> (34)..(34)
<223> The 'Xaa' at location 34 stands for Lys, Asn, Arg, Ser, Thr, Ile,
Met, Glu, Asp, Gly, Ala, Val, Gln, His, Pro, Leu, a stop codon,
Tyr, Trp, Cys, or Phe.

<220>
<221> misc_feature
<222> (35)..(35)
<223> The 'Xaa' at location 35 stands for Lys, Asn, Arg, Ser, Thr, Ile,
Met, Glu, Asp, Gly, Ala, Val, Gln, His, Pro, Leu, a stop codon,
Tyr, Trp, Cys, or Phe.

<220>
<221> misc_feature
<222> (36)..(36)
<223> The 'Xaa' at location 36 stands for Lys, Asn, Arg, Ser, Thr, Ile,
Met, Glu, Asp, Gly, Ala, Val, Gln, His, Pro, Leu, a stop codon,
Tyr, Trp, Cys, or Phe.

<220>
<221> misc_feature
<222> (37)..(37)
<223> The 'Xaa' at location 37 stands for Lys, Asn, Arg, Ser, Thr, Ile,
Met, Glu, Asp, Gly, Ala, Val, Gln, His, Pro, Leu, a stop codon,
Tyr, Trp, Cys, or Phe.

<220>
<221> misc_feature
<222> (38)..(38)
<223> The 'Xaa' at location 38 stands for Lys, Asn, Arg, Ser, Thr, Ile,
Met, Glu, Asp, Gly, Ala, Val, Gln, His, Pro, Leu, a stop codon,
Tyr, Trp, Cys, or Phe.

<220>
<221> misc_feature
<222> (39)..(39)
<223> The 'Xaa' at location 39 stands for Lys, Asn, Arg, Ser, Thr, Ile,
Met, Glu, Asp, Gly, Ala, Val, Gln, His, Pro, Leu, a stop codon,
Tyr, Trp, Cys, or Phe.

<220>
<221> misc_feature
<222> (40)..(40)
<223> The 'Xaa' at location 40 stands for Lys, Asn, Arg, Ser, Thr, Ile,
Met, Glu, Asp, Gly, Ala, Val, Gln, His, Pro, Leu, a stop codon,
Tyr, Trp, Cys, or Phe.

<220>
<221> misc_feature
<222> (41)..(41)
<223> The 'Xaa' at location 41 stands for Lys, Asn, Arg, Ser, Thr, Ile,
Met, Glu, Asp, Gly, Ala, Val, Gln, His, Pro, Leu, a stop codon,
Tyr, Trp, Cys, or Phe.

<220>

<221> misc_feature
 <222> (42)..(42)
 <223> The 'Xaa' at location 42 stands for Lys, Asn, Arg, Ser, Thr, Ile,
 Met, Glu, Asp, Gly, Ala, Val, Gln, His, Pro, Leu, a stop codon,
 Tyr, Trp, Cys, or Phe.

<220>
 <221> misc_feature
 <222> (43)..(43)
 <223> The 'Xaa' at location 43 stands for Lys, Asn, Arg, Ser, Thr, Ile,
 Met, Glu, Asp, Gly, Ala, Val, Gln, His, Pro, Leu, a stop codon,
 Tyr, Trp, Cys, or Phe.

<220>
 <221> misc_feature
 <222> (44)..(44)
 <223> The 'Xaa' at location 44 stands for Lys, Asn, Arg, Ser, Thr, Ile,
 Met, Glu, Asp, Gly, Ala, Val, Gln, His, Pro, Leu, a stop codon,
 Tyr, Trp, Cys, or Phe.

<220>
 <221> misc_feature
 <222> (45)..(45)
 <223> The 'Xaa' at location 45 stands for Lys, Asn, Arg, Ser, Thr, Ile,
 Met, Glu, Asp, Gly, Ala, Val, Gln, His, Pro, Leu, a stop codon,
 Tyr, Trp, Cys, or Phe.

<220>
 <221> misc_feature
 <222> (46)..(46)
 <223> The 'Xaa' at location 46 stands for Lys, Asn, Arg, Ser, Thr, Ile,
 Met, Glu, Asp, Gly, Ala, Val, Gln, His, Pro, Leu, a stop codon,
 Tyr, Trp, Cys, or Phe.

<220>
 <221> misc_feature
 <222> (47)..(47)
 <223> The 'Xaa' at location 47 stands for Lys, Asn, Arg, Ser, Thr, Ile,
 Met, Glu, Asp, Gly, Ala, Val, Gln, His, Pro, Leu, a stop codon,
 Tyr, Trp, Cys, or Phe.

<220>
 <221> misc_feature
 <222> (48)..(48)
 <223> The 'Xaa' at location 48 stands for Lys, Asn, Arg, Ser, Thr, Ile,
 Met, Glu, Asp, Gly, Ala, Val, Gln, His, Pro, Leu, a stop codon,
 Tyr, Trp, Cys, or Phe.

<220>
 <221> misc_feature
 <222> (49)..(49)
 <223> The 'Xaa' at location 49 stands for Lys, Asn, Arg, Ser, Thr, Ile,
 Met, Glu, Asp, Gly, Ala, Val, Gln, His, Pro, Leu, a stop codon,
 Tyr, Trp, Cys, or Phe.

<220>
 <221> misc_feature

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<222> (50)..(50)
<223> The 'Xaa' at location 50 stands for Lys, Asn, Arg, Ser, Thr, Ile,
      Met, Glu, Asp, Gly, Ala, Val, Gln, His, Pro, Leu, a stop codon,
      Tyr, Trp, Cys, or Phe.

<220>
<221> misc_feature
<222> (51)..(51)
<223> The 'Xaa' at location 51 stands for Lys, Asn, Arg, Ser, Thr, Ile,
      Met, Glu, Asp, Gly, Ala, Val, Gln, His, Pro, Leu, a stop codon,
      Tyr, Trp, Cys, or Phe.

<220>
<221> misc_feature
<222> (52)..(52)
<223> The 'Xaa' at location 52 stands for Lys, Asn, Arg, Ser, Thr, Ile,
      Met, Glu, Asp, Gly, Ala, Val, Gln, His, Pro, Leu, a stop codon,
      Tyr, Trp, Cys, or Phe.

<220>
<221> misc_feature
<222> (53)..(53)
<223> The 'Xaa' at location 53 stands for Lys, Asn, Arg, Ser, Thr, Ile,
      Met, Glu, Asp, Gly, Ala, Val, Gln, His, Pro, Leu, a stop codon,
      Tyr, Trp, Cys, or Phe.

<220>
<221> misc_feature
<222> (54)..(54)
<223> The 'Xaa' at location 54 stands for Lys, Asn, Arg, Ser, Thr, Ile,
      Met, Glu, Asp, Gly, Ala, Val, Gln, His, Pro, Leu, a stop codon,
      Tyr, Trp, Cys, or Phe.

<220>
<221> misc_feature
<222> (55)..(55)
<223> The 'Xaa' at location 55 stands for Lys, Asn, Arg, Ser, Thr, Ile,
      Met, Glu, Asp, Gly, Ala, Val, Gln, His, Pro, Leu, a stop codon,
      Tyr, Trp, Cys, or Phe.

<220>
<221> misc_feature
<222> (56)..(56)
<223> The 'Xaa' at location 56 stands for Lys, Asn, Arg, Ser, Thr, Ile,
      Met, Glu, Asp, Gly, Ala, Val, Gln, His, Pro, Leu, a stop codon,
      Tyr, Trp, Cys, or Phe.

<220>
<221> misc_feature
<222> (324)..(324)
<223> The 'Xaa' at location 324 stands for Glu, or Asp.

<220>
<221> misc_feature
<222> (82)..(168)
<223> n = A, C, T, or G

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<400> 76

Met Ser Arg Cys Phe Pro Tyr Pro Pro Gly Tyr Val Arg Asn Pro
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Val Ala Val Ala Glu Pro Glu Ser Thr Ala Lys Xaa Xaa Xaa Xaa Xaa
20 25 30

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
35 40 45

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Ser Lys His Ser His Lys Lys Arg
50 55 60

Lys Leu Glu Asp Val Ile Lys Ala Glu Gln Val Pro Lys Arg Val Pro
65 70 75 80

Lys Glu Ser Val Glu Gln Leu Glu Lys Ser Gly Leu Ser Glu Glu His
85 90 95

Gly Ala Pro Ser Phe Val His Thr Ile Arg Asp Ser Pro Glu Ser Ser
100 105 110

Gln Asp Ser Gly Lys Arg Arg Lys Val Val Leu Ser Ser Pro Ser Gln
115 120 125

Pro Lys Asn Gly Asn Ile Leu Arg Phe Lys Ile Lys Ser Ser Gln Asp
130 135 140

Pro Gln Ser Ala Val Leu Glu Lys Pro Arg Val Leu Glu Gln Pro Leu
145 150 155 160

Val Gln Gln Met Gly Ser Gly Ser Ser Leu Ser Gly Lys Gln Asn Ser
165 170 175

Ile His His Lys Met Asn Val Arg Ser Thr Ser Gly Gln Arg Arg Val
180 185 190

Asn Gly Asp Ser Gln Ala Val Gln Lys Cys Leu Ile Thr Glu Ser Pro
195 200 205

Ala Lys Thr Met Gln Arg Leu Val Pro Gln Pro Ala Ala Lys Val Thr
210 215 220

1007304-2406200T

His Pro Val Asp Pro Gln Ser Ala Val Lys Val Pro Val Gly Arg Ser
225 230 235 240

Gly Leu Pro Leu Lys Ser Ser Gly Ser Val Asp Pro Ser Pro Ala Arg
245 250 255

Val Met Arg Arg Phe Asp Pro Pro Pro Val Lys Met Met Ser Gln Arg
260 265 270

Val His His Pro Ala Ser Met Val Ser Gln Lys Val Asp Pro Pro Phe
275 280 285

Pro Lys Val Leu His Lys Glu Thr Gly Ser Val Val Arg Leu Pro Glu
290 295 300

Ala Thr Arg Pro Thr Val Leu Gln Lys Pro Lys Asp Leu Pro Ala Ile
305 310 315 320

Lys Gln Gln Xaa Ile Arg Thr Ser Ser Ser Lys Glu Glu Pro Cys Phe
325 330 335

Ser Gly Arg Asn Ala Glu Ala Val Gln Val Gln Asp Thr Lys Leu Ser
340 345 350

Arg Ser Asp Met Lys Lys Ile Arg Lys Ala Glu Lys Lys Asp Lys Lys
355 360 365

Phe Arg Asp Leu Phe Val Thr Trp Asn Pro Val Leu Ile Glu Asn Glu
370 375 380

Gly Ser Asp Leu Gly Asp Glu Asp Trp Leu Phe Ser Ser Lys Arg Asn
385 390 395 400

Ser Asp Ala Ile Met Val Gln Ser Arg Ala Thr Asp Ser Ser Val Pro
405 410 415

Ile His Pro Met Val Gln Gln Lys Pro Ser Leu Gln Pro Arg Ala Thr
420 425 430

Phe Leu Pro Asp Leu Asn Met Tyr Gln Leu Pro Tyr
435 440

<210> 77
 <211> 86
 <212> DNA
 <213> Zea mays parviglumis strain Wilkes

<400> 77
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 caccggggta cgtgcggaac ccagtg 86

<210> 78
 <211> 1347
 <212> DNA
 <213> Zea mays parviglumis strain Wilkes

<220>
 <221> misc_feature
 <222> (52)..(81)
 <223> N = A, C, G, or T

<220>
 <221> CDS
 <222> (1)..(1347)
 <223>

<400> 78
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 1 5 10 15
 gtg nnn nnn nnn nnn nnn nnn nnn nnn nnn nnn ctc ctg aaa gaa aag 96
 Val Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Leu Leu Lys Glu Lys
 20 25 30
 gaa aag gcc gaa aag aag aaa gag aaa agg agt gac agg aaa gct ccc 144
 Glu Lys Ala Glu Lys Lys Lys Glu Lys Arg Ser Asp Arg Lys Ala Pro
 35 40 45
 aag cag tgt gag acg tcc aaa cat tca aag cac agc cat aag aag aga 192
 Lys Gln Cys Glu Thr Ser Lys His Ser Lys His Ser His Lys Lys Arg
 50 55 60
 aag ctt gaa gat gtc atc aaa gct gag cag ggt ccc aaa aga gta ccc 240
 Lys Leu Glu Asp Val Ile Lys Ala Glu Gln Gly Pro Lys Arg Val Pro
 65 70 75 80
 aaa gaa tca gtt gag cag ttg gag aag agt gga ctc tca gaa gag cat 288
 Lys Glu Ser Val Glu Gln Leu Glu Lys Ser Gly Leu Ser Glu Glu His
 85 90 95
 gga gct cct tct ttt gta cat acg ata cgt gac tct cct gag agc tca 336
 Gly Ala Pro Ser Phe Val His Thr Ile Arg Asp Ser Pro Glu Ser Ser
 100 105 110

cag gac agc ggc aag aga cga aag gtt gtc ctg tcc agt cct agc caa Gln Asp Ser Gly Lys Arg Arg Lys Val Val Leu Ser Ser Pro Ser Gln 115 120 125	384
cct aag aat gga aac att ctt cgc ttc aag att aaa agt agt caa gat Pro Lys Asn Gly Asn Ile Leu Arg Phe Lys Ile Lys Ser Ser Gln Asp 130 135 140	432
ccc caa tca gct gtt ctg gag aaa cca agg gtt ctt gag caa cca ttg Pro Gln Ser Ala Val Leu Glu Lys Pro Arg Val Leu Glu Gln Pro Leu 145 150 155 160	480
gtc caa caa atg gga tca ggt tca tcc ctg tcg ggc aag caa aat tca Val Gln Gln Met Gly Ser Gly Ser Ser Leu Ser Gly Lys Gln Asn Ser 165 170 175	528
atc cat cat aag atg aat gtg aga tct acc tct ggt cag cgg agg gtc Ile His His Lys Met Asn Val Arg Ser Thr Ser Gly Gln Arg Arg Val 180 185 190	576
aat ggt gac tcc caa gca gta caa aaa tgt ttg att aca gaa tcc ccg Asn Gly Asp Ser Gln Ala Val Gln Lys Cys Leu Ile Thr Glu Ser Pro 195 200 205	624
gca aag acc atg cag aga ctt gtc ccc cag cct gca gct aag gtc aca Ala Lys Thr Met Gln Arg Leu Val Pro Gln Pro Ala Ala Lys Val Thr 210 215 220	672
cat cct gtt gat ccc cag tca gct gtt aag gtg cca gtt gga aga tcg His Pro Val Asp Pro Gln Ser Ala Val Lys Val Pro Val Gly Arg Ser 225 230 235 240	720
ggc cta cct ctg aag tct tcg gga agt gtg gac cct tcg cct gct aga Gly Leu Pro Leu Lys Ser Ser Gly Ser Val Asp Pro Ser Pro Ala Arg 245 250 255	768
gtt atg aga aga ttt gat cct cca cct gtt aag atg atg tca cag aga Val Met Arg Arg Phe Asp Pro Pro Pro Val Lys Met Met Ser Gln Arg 260 265 270	816
gtt cac cat cca gct tcc atg gtg tcg cag aaa gtt gat cct ccg ttt Val His His Pro Ala Ser Met Val Ser Gln Lys Val Asp Pro Pro Phe 275 280 285	864
ccg aag gta tta cat aag gaa acc gga tct gtt gtt cgc cta cca gaa Pro Lys Val Leu His Lys Glu Thr Gly Ser Val Val Arg Leu Pro Glu 290 295 300	912
gct acc cgg cct act gtt ctt caa aaa ccc aag gac ttg cct gct atc Ala Thr Arg Pro Thr Val Leu Gln Lys Pro Lys Asp Leu Pro Ala Ile 305 310 315 320	960
aag cag cag gat atc agg acc tct tcc tca aaa gaa gag ccc tgc ttc Lys Gln Gln Asp Ile Arg Thr Ser Ser Ser Lys Glu Glu Pro Cys Phe 325 330 335	1008
tct ggt agg aat gca gaa gca gtt caa gtg caa gat act aag ctc tcc	1056

Ser Gly Arg Asn Ala Glu Ala Val Gln Val Gln Asp Thr Lys Leu Ser	
340 345 350	
cgg tca gac atg aag aaa atc cgc aaa gct gag aaa aaa gat aag aag	1104
Arg Ser Asp Met Lys Lys Ile Arg Lys Ala Glu Lys Lys Asp Lys Lys	
355 360 365	
ttc aga gat ctg ttt gtt acc tgg aat ccg gta ttg ata gag aat gaa	1152
Phe Arg Asp Leu Phe Val Thr Trp Asn Pro Val Leu Ile Glu Asn Glu	
370 375 380	
ggt tca gat ctt ggt gat gaa gac tgg ctg ttc agc agt aaa agg aac	1200
Gly Ser Asp Leu Gly Asp Glu Asp Trp Leu Phe Ser Ser Lys Arg Asn	
385 390 395 400	
tcc gat gct atc atg gtt caa agc aga gct act gat agt tca gtg ccg	1248
Ser Asp Ala Ile Met Val Gln Ser Arg Ala Thr Asp Ser Ser Val Pro	
405 410 415	
atc cat cca atg gtg cag cag aag cct tct tta caa ccc agg gca aca	1296
Ile His Pro Met Val Gln Gln Lys Pro Ser Leu Gln Pro Arg Ala Thr	
420 425 430	
ttt ttg ccg gac ctt aat atg tac cag ctg cca tat gtc gta cca ttt	1344
Phe Leu Pro Asp Leu Asn Met Tyr Gln Leu Pro Tyr Val Val Pro Phe	
435 440 445	
taa	1347

<210> 79
 <211> 448
 <212> PRT
 <213> Zea mays parviglumis strain Wilkes

<220>
 <221> misc_feature
 <222> (18)..(18)
 <223> The 'Xaa' at location 18 stands for Lys, Asn, Arg, Ser, Thr, Ile, Met, Glu, Asp, Gly, Ala, Val, Gln, His, Pro, Leu, a stop codon, Tyr, Trp, Cys, or Phe.

<220>
 <221> misc_feature
 <222> (19)..(19)
 <223> The 'Xaa' at location 19 stands for Lys, Asn, Arg, Ser, Thr, Ile, Met, Glu, Asp, Gly, Ala, Val, Gln, His, Pro, Leu, a stop codon, Tyr, Trp, Cys, or Phe.

<220>
 <221> misc_feature
 <222> (20)..(20)
 <223> The 'Xaa' at location 20 stands for Lys, Asn, Arg, Ser, Thr, Ile, Met, Glu, Asp, Gly, Ala, Val, Gln, His, Pro, Leu, a stop codon, Tyr, Trp, Cys, or Phe.

<220>

200904.04062001

<221> misc_feature
 <222> (21)..(21)
 <223> The 'Xaa' at location 21 stands for Lys, Asn, Arg, Ser, Thr, Ile, Met, Glu, Asp, Gly, Ala, Val, Gln, His, Pro, Leu, a stop codon, Tyr, Trp, Cys, or Phe.

<220>
 <221> misc_feature
 <222> (22)..(22)
 <223> The 'Xaa' at location 22 stands for Lys, Asn, Arg, Ser, Thr, Ile, Met, Glu, Asp, Gly, Ala, Val, Gln, His, Pro, Leu, a stop codon, Tyr, Trp, Cys, or Phe.

<220>
 <221> misc_feature
 <222> (23)..(23)
 <223> The 'Xaa' at location 23 stands for Lys, Asn, Arg, Ser, Thr, Ile, Met, Glu, Asp, Gly, Ala, Val, Gln, His, Pro, Leu, a stop codon, Tyr, Trp, Cys, or Phe.

<220>
 <221> misc_feature
 <222> (24)..(24)
 <223> The 'Xaa' at location 24 stands for Lys, Asn, Arg, Ser, Thr, Ile, Met, Glu, Asp, Gly, Ala, Val, Gln, His, Pro, Leu, a stop codon, Tyr, Trp, Cys, or Phe.

<220>
 <221> misc_feature
 <222> (25)..(25)
 <223> The 'Xaa' at location 25 stands for Lys, Asn, Arg, Ser, Thr, Ile, Met, Glu, Asp, Gly, Ala, Val, Gln, His, Pro, Leu, a stop codon, Tyr, Trp, Cys, or Phe.

<220>
 <221> misc_feature
 <222> (26)..(26)
 <223> The 'Xaa' at location 26 stands for Lys, Asn, Arg, Ser, Thr, Ile, Met, Glu, Asp, Gly, Ala, Val, Gln, His, Pro, Leu, a stop codon, Tyr, Trp, Cys, or Phe.

<220>
 <221> misc_feature
 <222> (27)..(27)
 <223> The 'Xaa' at location 27 stands for Lys, Asn, Arg, Ser, Thr, Ile, Met, Glu, Asp, Gly, Ala, Val, Gln, His, Pro, Leu, a stop codon, Tyr, Trp, Cys, or Phe.

<220>
 <221> misc_feature
 <222> (52)..(81)
 <223> N = A, C, G, or T

<400> 79

Met Ser Arg Cys Phe Pro Tyr Pro Pro Pro Gly Tyr Val Arg Asn Pro
 1 5 10 15

Val Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Leu Leu Lys Glu Lys
20 25 30

Glu Lys Ala Glu Lys Lys Lys Glu Lys Arg Ser Asp Arg Lys Ala Pro
35 40 45

Lys Gln Cys Glu Thr Ser Lys His Ser Lys His Ser His Lys Lys Arg
50 55 60

Lys Leu Glu Asp Val Ile Lys Ala Glu Gln Gly Pro Lys Arg Val Pro
65 70 75 80

Lys Glu Ser Val Glu Gln Leu Glu Lys Ser Gly Leu Ser Glu Glu His
85 90 95

Gly Ala Pro Ser Phe Val His Thr Ile Arg Asp Ser Pro Glu Ser Ser
100 105 110

Gln Asp Ser Gly Lys Arg Arg Lys Val Val Leu Ser Ser Pro Ser Gln
115 120 125

Pro Lys Asn Gly Asn Ile Leu Arg Phe Lys Ile Lys Ser Ser Gln Asp
130 135 140

Pro Gln Ser Ala Val Leu Glu Lys Pro Arg Val Leu Glu Gln Pro Leu
145 150 155 160

Val Gln Gln Met Gly Ser Gly Ser Ser Leu Ser Gly Lys Gln Asn Ser
165 170 175

Ile His His Lys Met Asn Val Arg Ser Thr Ser Gly Gln Arg Arg Val
180 185 190

Asn Gly Asp Ser Gln Ala Val Gln Lys Cys Leu Ile Thr Glu Ser Pro
195 200 205

Ala Lys Thr Met Gln Arg Leu Val Pro Gln Pro Ala Ala Lys Val Thr
210 215 220

His Pro Val Asp Pro Gln Ser Ala Val Lys Val Pro Val Gly Arg Ser
225 230 235 240

2006T20 21406200T

Gly Leu Pro Leu Lys Ser Ser Gly Ser Val Asp Pro Ser Pro Ala Arg
245 250 255

Val Met Arg Arg Phe Asp Pro Pro Pro Val Lys Met Met Ser Gln Arg
260 265 270

Val His His Pro Ala Ser Met Val Ser Gln Lys Val Asp Pro Pro Phe
275 280 285

Pro Lys Val Leu His Lys Glu Thr Gly Ser Val Val Arg Leu Pro Glu
290 295 300

Ala Thr Arg Pro Thr Val Leu Gln Lys Pro Lys Asp Leu Pro Ala Ile
305 310 315 320

Lys Gln Gln Asp Ile Arg Thr Ser Ser Ser Lys Glu Glu Pro Cys Phe
325 330 335

Ser Gly Arg Asn Ala Glu Ala Val Gln Val Gln Asp Thr Lys Leu Ser
340 345 350

Arg Ser Asp Met Lys Lys Ile Arg Lys Ala Glu Lys Lys Asp Lys Lys
355 360 365

Phe Arg Asp Leu Phe Val Thr Trp Asn Pro Val Leu Ile Glu Asn Glu
370 375 380

Gly Ser Asp Leu Gly Asp Glu Asp Trp Leu Phe Ser Ser Lys Arg Asn
385 390 395 400

Ser Asp Ala Ile Met Val Gln Ser Arg Ala Thr Asp Ser Ser Val Pro
405 410 415

Ile His Pro Met Val Gln Gln Lys Pro Ser Leu Gln Pro Arg Ala Thr
420 425 430

Phe Leu Pro Asp Leu Asn Met Tyr Gln Leu Pro Tyr Val Val Pro Phe
435 440 445

<210> 80
<211> 225
<212> DNA
<213> Zea diploperennis

<400> 80
 agcgcggtcg accgtcggcc atgtcgaggt gcttccccta cccgccaccg gggtagctgc 60
 ggaacccagt ggccgtggcc gagccggagt cgaccgctaa ggtttggtga accttcggat 120
 ttacacacgc acgtgccaga tcgtttgttc aatctgtagg ttttgccgcg atctgtggtt 180
 tgcgcgtgcg tgatgtgggt attgcccgtg ccttgaaagc taacc 225

<210> 81
 <211> 1672
 <212> DNA
 <213> Zea diploperennis

<400> 81
 agcccathtt tagttttatt gttctgtaga gtatgcattg ttgcaggctt taactgttgt 60
 cagggaagta acgtgttcaa catgattgta aacgaatata attctgttgc taactgtgta 120
 atgatgagaa ggataattga ataatctttg tgaagtatta ctgtctgaac tgtacgcaaa 180
 tgctacattc attctttgtg ttcgtgtaaa tatcattata cataaaaaatg ctgcattgca 240
 ttcccgtcgt ccgttctaaa tcagaactga cgattgctct ggtggctgaa gtccttgaaa 300
 gaaaaggaaa aggccgaaaa gaagaaagag aaaaggagtg acaggaaagc tcccaagcag 360
 tgtgagacgt ccaaacactc aaagcacagc cataagaaga gaaagcttga agatgtcatc 420
 aaagctgagc aggggtccaa aagagtacc aaagaatcag ttgagcagtt ggagaagagt 480
 ggactctcag aagagcatgg agctccttct tttgtacata cgatacgtga ctctcctgag 540
 agctcacagg acagcggcaa gagacgaaag gttgtcctgt ccagtcctag ccaacctaa 600
 aatggtgaga ctattctctt gtttttgcta ttctgattga ttttttatta tagaagaaat 660
 caatcacttg ttcaggattt tattcatccc aacttgattt tacaggaaac attcttcgct 720
 tcaagattaa aagtagtcaa gatccccaat cagctgttct ggagaaacca agggttcttg 780
 agcaaccatt ggtccaacaa atgggatcag gttcatccct gtcgggcaag caaaattcaa 840
 tccatcataa gatgaatgtg agatctacct ctggtcagcg gagggccaat ggtgactcgc 900
 aagcagtaca aaaatgtttg attacagaat ccccggaacaa gaccatgcag agacttgtcc 960
 cccagcctgc agctaaggct acacatcctg ttgatcccca gtcagctggt aaggtgccag 1020
 ttggaaggct gggcctacct ctcaagtttt cgggaagtat ggacccttcg cctgctagag 1080
 ttatgggaag atttgatcct ccacctgtta agatgatgtc acagagagtt caccatccag 1140
 cttccatggt gtcgcagaaa gttgatcctc cgttaccgaa ggtattacat aaggaaaccg 1200

gatctgttgt tcgcctacca gaagctaccc ggcctactgt tcttcaaaaa cccaaggact 1260
 tgcctgctat caagcagcag cagatcagga cctcttcctc aaaagaagag ccctgcttct 1320
 ctggtaggaa tgcagaagca gttcaagtgc atgatactaa gctctcccgg tcagatatga 1380
 agaaaatccg caaagctgag aaaaaagata agaagttcag agatctgttt gttacctgga 1440
 atccggtatt gatagagaat gaaggttcag atcttggtga tgaagactgg ctgttcagca 1500
 gtaaaaggaa ctccgatgct atcatgggtc aaagcagagc tactgatagt tcagtgccga 1560
 tccatccaat kgtgcagcag aaaccttctt tacaaccag ggcaacattt ttgccggacc 1620
 ttaatatgta ccagctgccca tatgtcgtac cattttaaac atctgtcgag gt 1672

<210> 82
 <211> 1347
 <212> DNA
 <213> Zea diploperennis

<220>
 <221> CDS
 <222> (1)..(1347)
 <223>

<400> 82
 atg tcg agg tgc ttc ccc tac ccg cca ccg ggg tac gtg cgg aac cca 48
 Met Ser Arg Cys Phe Pro Tyr Pro Pro Pro Gly Tyr Val Arg Asn Pro
 1 5 10 15
 gtg gcc gtg gcc gag ccg gag tcg acc gct aag ctc ctg aaa gaa aag 96
 Val Ala Val Ala Glu Pro Glu Ser Thr Ala Lys Leu Leu Lys Glu Lys
 20 25 30
 gaa aag gcc gaa aag aag aaa gag aaa agg agt gac agg aaa gct ccc 144
 Glu Lys Ala Glu Lys Lys Lys Glu Lys Arg Ser Asp Arg Lys Ala Pro
 35 40 45
 aag cag tgt gag acg tcc aaa cac tca aag cac agc cat aag aag aga 192
 Lys Gln Cys Glu Thr Ser Lys His Ser Lys His Ser His Lys Lys Arg
 50 55 60
 aag ctt gaa gat gtc atc aaa gct gag cag ggt ccc aaa aga gta ccc 240
 Lys Leu Glu Asp Val Ile Lys Ala Glu Gln Gly Pro Lys Arg Val Pro
 65 70 75 80
 aaa gaa tca gtt gag cag ttg gag aag agt gga ctc tca gaa gag cat 288
 Lys Glu Ser Val Glu Gln Leu Glu Lys Ser Gly Leu Ser Glu Glu His
 85 90 95
 gga gct cct tct ttt gta cat acg ata cgt gac tct cct gag agc tca 336
 Gly Ala Pro Ser Phe Val His Thr Ile Arg Asp Ser Pro Glu Ser Ser
 100 105 110

20051220 21064001

Ser Gly Arg Asn Ala Glu Ala Val Gln Val His Asp Thr Lys Leu Ser
340 345 350

cgg tca gat atg aag aaa atc cgc aaa gct gag aaa aaa gat aag aag 1104
Arg Ser Asp Met Lys Lys Ile Arg Lys Ala Glu Lys Lys Asp Lys Lys
355 360 365

ttc aga gat ctg ttt gtt acc tgg aat ccg gta ttg ata gag aat gaa 1152
Phe Arg Asp Leu Phe Val Thr Trp Asn Pro Val Leu Ile Glu Asn Glu
370 375 380

ggc tca gat ctt ggt gat gaa gac tgg ctg ttc agc agt aaa agg aac 1200
Gly Ser Asp Leu Gly Asp Glu Asp Trp Leu Phe Ser Ser Lys Arg Asn
385 390 395 400

tcc gat gct atc atg gtt caa agc aga gct act gat agt tca gtg ccg 1248
Ser Asp Ala Ile Met Val Gln Ser Arg Ala Thr Asp Ser Ser Val Pro
405 410 415

atc cat cca atk gtg cag cag aaa cct tct tta caa ccc agg gca aca 1296
Ile His Pro Xaa Val Gln Gln Lys Pro Ser Leu Gln Pro Arg Ala Thr
420 425 430

ttt ttg ccg gac ctt aat atg tac cag ctg cca tat gtc gta cca ttt 1344
Phe Leu Pro Asp Leu Asn Met Tyr Gln Leu Pro Tyr Val Val Pro Phe
435 440 445

taa 1347

<210> 83
<211> 448
<212> PRT
<213> Zea diploperennis

<220>
<221> misc_feature
<222> (420)..(420)
<223> The 'Xaa' at location 420 stands for Met, or Ile.

<400> 83

Met Ser Arg Cys Phe Pro Tyr Pro Pro Gly Tyr Val Arg Asn Pro
1 5 10 15

Val Ala Val Ala Glu Pro Glu Ser Thr Ala Lys Leu Leu Lys Glu Lys
20 25 30

Glu Lys Ala Glu Lys Lys Lys Glu Lys Arg Ser Asp Arg Lys Ala Pro
35 40 45

Lys Gln Cys Glu Thr Ser Lys His Ser Lys His Ser His Lys Lys Arg
50 55 60

Lys Leu Glu Asp Val Ile Lys Ala Glu Gln Gly Pro Lys Arg Val Pro
65 70 75 80

Lys Glu Ser Val Glu Gln Leu Glu Lys Ser Gly Leu Ser Glu Glu His
85 90 95

Gly Ala Pro Ser Phe Val His Thr Ile Arg Asp Ser Pro Glu Ser Ser
100 105 110

Gln Asp Ser Gly Lys Arg Arg Lys Val Val Leu Ser Ser Pro Ser Gln
115 120 125

Pro Lys Asn Gly Asn Ile Leu Arg Phe Lys Ile Lys Ser Ser Gln Asp
130 135 140

Pro Gln Ser Ala Val Leu Glu Lys Pro Arg Val Leu Glu Gln Pro Leu
145 150 155 160

Val Gln Gln Met Gly Ser Gly Ser Ser Leu Ser Gly Lys Gln Asn Ser
165 170 175

Ile His His Lys Met Asn Val Arg Ser Thr Ser Gly Gln Arg Arg Val
180 185 190

Asn Gly Asp Ser Gln Ala Val Gln Lys Cys Leu Ile Thr Glu Ser Pro
195 200 205

Ala Lys Thr Met Gln Arg Leu Val Pro Gln Pro Ala Ala Lys Val Thr
210 215 220

His Pro Val Asp Pro Gln Ser Ala Val Lys Val Pro Val Gly Arg Ser
225 230 235 240

Gly Leu Pro Leu Lys Phe Ser Gly Ser Met Asp Pro Ser Pro Ala Arg
245 250 255

Val Met Gly Arg Phe Asp Pro Pro Pro Val Lys Met Met Ser Gln Arg
260 265 270

Val His His Pro Ala Ser Met Val Ser Gln Lys Val Asp Pro Pro Leu
275 280 285

Pro Lys Val Leu His Lys Glu Thr Gly Ser Val Val Arg Leu Pro Glu
290 295 300

Ala Thr Arg Pro Thr Val Leu Gln Lys Pro Lys Asp Leu Pro Ala Ile
305 310 315 320

Lys Gln Gln Gln Ile Arg Thr Ser Ser Ser Lys Glu Glu Pro Cys Phe
325 330 335

Ser Gly Arg Asn Ala Glu Ala Val Gln Val His Asp Thr Lys Leu Ser
340 345 350

Arg Ser Asp Met Lys Lys Ile Arg Lys Ala Glu Lys Lys Asp Lys Lys
355 360 365

Phe Arg Asp Leu Phe Val Thr Trp Asn Pro Val Leu Ile Glu Asn Glu
370 375 380

Gly Ser Asp Leu Gly Asp Glu Asp Trp Leu Phe Ser Ser Lys Arg Asn
385 390 395 400

Ser Asp Ala Ile Met Val Gln Ser Arg Ala Thr Asp Ser Ser Val Pro
405 410 415

Ile His Pro Xaa Val Gln Gln Lys Pro Ser Leu Gln Pro Arg Ala Thr
420 425 430

Phe Leu Pro Asp Leu Asn Met Tyr Gln Leu Pro Tyr Val Val Pro Phe
435 440 445

<210> 84
<211> 2423
<212> DNA
<213> Zea luxurians

<400> 84
ggccatgtcg aggtgcttcc cctacccgcc accggggtac gtgcggaacc cagtggccgt 60
ggccgagccg gagtgcaccg ctaagggttg ttgaaccttc ggatttacac acgcacgtgc 120
cagatcgttt ggtcaatctg ttggttttgc gcggatctgt ggtttgcgcg tgcgtgatgt 180
gggtattgcc cgtgccttga aagctaaccg agatgaggaa gtgtatggat cttgttttagc 240
tgcacgaggt cctccaaatc gattgaaaaa tttaagttgg atggccggtg ggccaagatt 300
gggttagtcc ggtttttgat aactgggtacc atggttatcg gggacattga acagaacggt 360

agaacatcaa attcgattca aaactgtgct agatttgcac atttagtcgc cctaagatta	420
cgtggacgtg ggtgggccga attgggtgtt gttgtatgat ggttggaata tgagccattt	480
agtgttccg tgactggcca aatatttttg tttctcaaat ttttctttga aaaactgttt	540
gtcgagcgtc aattcttaat acagtatgtc gttatttttg gctaagcttg tgaaacaagg	600
gtcgtttgac atttgtactg tattaacctg atgttactct tctggttgac caaaggagtt	660
ttagaattat tttggctctg taaatcaata gcaactaaca ccatctattg tgcccatttt	720
tagttttgta tagttttgta tgcagtgttg caggctcttaa ctgttgctcag gaaagtaacg	780
tgttcacatg attgtaaacg aatacaattc tgttgctaac tgtgtaatga tgagaacgat	840
aattgaataa tctttgtgaa gtattactgt ctgaactgta cacaaatgct acattcattc	900
tttgtgttcg tgtaaagtc attatacata aaaaatgctg cattgcattc ccgtcgtccg	960
ttctaaatca gaactgacga ttgctctggt ggctgaagct cccgaaagaa aaggaaaagg	1020
ccgaaaagaa gaaagagaaa cggagtgcga ggaaagctcc caagcagtgt gagacgtcca	1080
aacattcaaa gcacatccat aagaagagaa agcttgaaga tgatcatcaa gctgggcagg	1140
gtcccaaaag agtaccctaa gaatcagttg agcagttgga gaagagtgga ctctcagaag	1200
agcatggagc tccttctttt gtacataaga tacgcgactc tcctgagagc tcacaggaca	1260
gcggcaagag acgaaagggt gtccctgtcca gtcctagcca acctaagaat ggtgagacta	1320
ttctcttggt tttgctattc tgattgattt tttattatag aagaaatcaa tcacttgttc	1380
cggattttat tcatcccaac ttgacatttt acaggaaaca ttcttcgctt caagattaaa	1440
agtaatcaag atccccaatc agctgttctg gagaaaccaa gggttcttga ccaaccattg	1500
gtccaacaaa tgggatcagg ttcatccctg tcgggcaagc aaaattcaat ccatcataag	1560
atgaatgtga gatctacctc tggtcagcgg aggggtcaatg gtgaatccca agcagtacaa	1620
aatgtttga ttacagaatc cccggcaaag accatgcaga gacttgtccc ccagcctgca	1680
gctaaggcca cacatcctgt tgatccccag tcagctgtta aggtgccagt tggaagatcg	1740
ggcctacctc tgaagttttc gggaagtgtg gacccttcgc ctgctagagt tatgggaaga	1800
tttgatctc cacctgttaa gatgatgtca cagagagttc accatccagc ttccatggtg	1860
tcgcagaaaag ttgatccctc gttaccgaag gtattacata aggaaaccgg atctgttggt	1920
cgctaccag aagctaccgg gcctactgtt cttcaaaaac ccaaggactt gcctgctatc	1980
aagcagcagg agatcaggac ctcttctctca aaagaagagc cctgcttctc tggtaggaat	2040

gcagaagcag ttcaagtgcg ggataactaag ctctcccggg cagatgtgaa gaaaatccgc 2100
aaagctgaga aaaaagataa gaagttcaga gatctgtttg ttacctggaa tccgggtgtg 2160
atagagaatg aaggttcaga tcttggtgat gaagactggc tgttcagcag taaaaggaac 2220
tccgatgcta tcatggctca aagcagagct actgatagtt cagtgccgat ccatccaatg 2280
gtgcagcaga agccttcttt gcaaccacag gcaacgtttt tgccggacct taatatctac 2340
cagctgccat atgtcgtacc attttaaaca tctgtcgagg tagatgagaa ttagatgaga 2400
tgttgggaga gagctgtgtg aac 2423

<210> 85
<211> 1347
<212> DNA
<213> Zea luxurians

<220>
<221> CDS
<222> (1)..(1347)
<223>

<400> 85
atg tcg agg tgc ttc ccc tac ccg cca ccg ggg tac gtg cgg aac cca 48
Met Ser Arg Cys Phe Pro Tyr Pro Pro Gly Tyr Val Arg Asn Pro
1 5 10 15
gtg gcc gtg gcc gag ccg gag tcg acc gct aag ctc ccg aaa gaa aag 96
Val Ala Val Ala Glu Pro Glu Ser Thr Ala Lys Leu Pro Lys Glu Lys
20 25 30
gaa aag gcc gaa aag aag aaa gag aaa ccg agt gac agg aaa gct ccc 144
Glu Lys Ala Glu Lys Lys Lys Glu Lys Arg Ser Asp Arg Lys Ala Pro
35 40 45
aag cag tgt gag acg tcc aaa cat tca aag cac atc cat aag aag aga 192
Lys Gln Cys Glu Thr Ser Lys His Ser Lys His Ile His Lys Lys Arg
50 55 60
aag ctt gaa gat gtc atc aaa gct ggg cag ggt ccc aaa aga gta ccc 240
Lys Leu Glu Asp Val Ile Lys Ala Gly Gln Gly Pro Lys Arg Val Pro
65 70 75 80
aaa gaa tca gtt gag cag ttg gag aag agt gga ctc tca gaa gag cat 288
Lys Glu Ser Val Glu Gln Leu Glu Lys Ser Gly Leu Ser Glu Glu His
85 90 95
gga gct cct tct ttt gta cat aag ata cgc gac tct cct gag agc tca 336
Gly Ala Pro Ser Phe Val His Lys Ile Arg Asp Ser Pro Glu Ser Ser
100 105 110
cag gac agc gcc aag aga cga aag gtt gtc ctg tcc agt cct agc caa 384
Gln Asp Ser Gly Lys Arg Arg Lys Val Val Leu Ser Ser Pro Ser Gln

115	120	125	
cct aag aat gga aac att ctt cgc ttc aag att aaa agt aat caa gat Pro Lys Asn Gly Asn Ile Leu Arg Phe Lys Ile Lys Ser Asn Gln Asp 130 135 140			432
ccc caa tca gct gtt ctg gag aaa cca agg gtt ctt gac caa cca ttg Pro Gln Ser Ala Val Leu Glu Lys Pro Arg Val Leu Asp Gln Pro Leu 145 150 155 160			480
gtc caa caa atg gga tca ggt tca tcc ctg tcg ggc aag caa aat tca Val Gln Gln Met Gly Ser Gly Ser Ser Leu Ser Gly Lys Gln Asn Ser 165 170 175			528
atc cat cat aag atg aat gtg aga tct acc tct ggt cag cgg agg gtc Ile His His Lys Met Asn Val Arg Ser Thr Ser Gly Gln Arg Arg Val 180 185 190			576
aat ggt gaa tcc caa gca gta caa aaa tgt ttg att aca gaa tcc ccg Asn Gly Glu Ser Gln Ala Val Gln Lys Cys Leu Ile Thr Glu Ser Pro 195 200 205			624
gca aag acc atg cag aga ctt gtc ccc cag cct gca gct aag gtc aca Ala Lys Thr Met Gln Arg Leu Val Pro Gln Pro Ala Ala Lys Val Thr 210 215 220			672
cat cct gtt gat ccc cag tca gct gtt aag gtg cca gtt gga aga tcg His Pro Val Asp Pro Gln Ser Ala Val Lys Val Pro Val Gly Arg Ser 225 230 235 240			720
ggc cta cct ctg aag ttt tcg gga agt gtg gac cct tcg cct gct aga Gly Leu Pro Leu Lys Phe Ser Gly Ser Val Asp Pro Ser Pro Ala Arg 245 250 255			768
gtt atg gga aga ttt gat cct cca cct gtt aag atg atg tca cag aga Val Met Gly Arg Phe Asp Pro Pro Pro Val Lys Met Met Ser Gln Arg 260 265 270			816
gtt cac cat cca gct tcc atg gtg tcg cag aaa gtt gat cct ccg tta Val His His Pro Ala Ser Met Val Ser Gln Lys Val Asp Pro Pro Leu 275 280 285			864
ccg aag gta tta cat aag gaa acc gga tct gtt gtt cgc cta cca gaa Pro Lys Val Leu His Lys Glu Thr Gly Ser Val Val Arg Leu Pro Glu 290 295 300			912
gct acc cgg cct act gtt ctt caa aaa ccc aag gac ttg cct gct atc Ala Thr Arg Pro Thr Val Leu Gln Lys Pro Lys Asp Leu Pro Ala Ile 305 310 315 320			960
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cgg tca gat gtg aag aaa atc cgc aaa gct gag aaa aaa gat aag aag 1104
 Arg Ser Asp Val Lys Lys Ile Arg Lys Ala Glu Lys Lys Asp Lys Lys
 355 360 365

ttc aga gat ctg ttt gtt acc tgg aat ccg gtg ttg ata gag aat gaa 1152
 Phe Arg Asp Leu Phe Val Thr Trp Asn Pro Val Leu Ile Glu Asn Glu
 370 375 380

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 Gly Ser Asp Leu Gly Asp Glu Asp Trp Leu Phe Ser Ser Lys Arg Asn
 385 390 395 400

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 Ser Asp Ala Ile Met Ala Gln Ser Arg Ala Thr Asp Ser Ser Val Pro
 405 410 415

atc cat cca atg gtg cag cag aag cct tct ttg caa ccc agg gca acg 1296
 Ile His Pro Met Val Gln Gln Lys Pro Ser Leu Gln Pro Arg Ala Thr
 420 425 430

ttt ttg ccg gac ctt aat atc tac cag ctg cca tat gtc gta cca ttt 1344
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taa 1347

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Glu Lys Ala Glu Lys Lys Lys Glu Lys Arg Ser Asp Arg Lys Ala Pro
 35 40 45

Lys Gln Cys Glu Thr Ser Lys His Ser Lys His Ile His Lys Lys Arg
 50 55 60

Lys Leu Glu Asp Val Ile Lys Ala Gly Gln Gly Pro Lys Arg Val Pro
 65 70 75 80

Lys Glu Ser Val Glu Gln Leu Glu Lys Ser Gly Leu Ser Glu Glu His
 85 90 95

Gly Ala Pro Ser Phe Val His Lys Ile Arg Asp Ser Pro Glu Ser Ser
 100 105 110

Gln Asp Ser Gly Lys Arg Arg Lys Val Val Leu Ser Ser Pro Ser Gln
 115 120 125

Pro Lys Asn Gly Asn Ile Leu Arg Phe Lys Ile Lys Ser Asn Gln Asp
 130 135 140

Pro Gln Ser Ala Val Leu Glu Lys Pro Arg Val Leu Asp Gln Pro Leu
 145 150 155 160

Val Gln Gln Met Gly Ser Gly Ser Ser Leu Ser Gly Lys Gln Asn Ser
 165 170 175

Ile His His Lys Met Asn Val Arg Ser Thr Ser Gly Gln Arg Arg Val
 180 185 190

Asn Gly Glu Ser Gln Ala Val Gln Lys Cys Leu Ile Thr Glu Ser Pro
 195 200 205

Ala Lys Thr Met Gln Arg Leu Val Pro Gln Pro Ala Ala Lys Val Thr
 210 215 220

His Pro Val Asp Pro Gln Ser Ala Val Lys Val Pro Val Gly Arg Ser
 225 230 235 240

Gly Leu Pro Leu Lys Phe Ser Gly Ser Val Asp Pro Ser Pro Ala Arg
 245 250 255

Val Met Gly Arg Phe Asp Pro Pro Pro Val Lys Met Met Ser Gln Arg
 260 265 270

Val His His Pro Ala Ser Met Val Ser Gln Lys Val Asp Pro Pro Leu
 275 280 285

Pro Lys Val Leu His Lys Glu Thr Gly Ser Val Val Arg Leu Pro Glu
 290 295 300

Ala Thr Arg Pro Thr Val Leu Gln Lys Pro Lys Asp Leu Pro Ala Ile
 305 310 315 320

Lys Gln Gln Glu Ile Arg Thr Ser Ser Ser Lys Glu Glu Pro Cys Phe
 325 330 335

Ser Gly Arg Asn Ala Glu Ala Val Gln Val Gln Asp Thr Lys Leu Ser
 340 345 350

Arg Ser Asp Val Lys Lys Ile Arg Lys Ala Glu Lys Lys Asp Lys Lys
 355 360 365

Phe Arg Asp Leu Phe Val Thr Trp Asn Pro Val Leu Ile Glu Asn Glu
 370 375 380

Gly Ser Asp Leu Gly Asp Glu Asp Trp Leu Phe Ser Ser Lys Arg Asn
 385 390 395 400

Ser Asp Ala Ile Met Ala Gln Ser Arg Ala Thr Asp Ser Ser Val Pro
 405 410 415

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21

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21

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<220>
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